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OM nucleic - nucleic search, using sw model

Run on: July 9, 2005, 18:07:47 ; Search time 8941 Seconds  
(without alignments)  
11597.602 Million cell updates/sec

Title: US-10-627-886-1  
Perfect score: 2140  
Sequence: 1 CTCCTTCTGCTGCGCCCTCT.....AAAAAAAAAAAAAAAAAAAA 2140

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sfc:\*  
12: gb\_ey:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2140	100.0	2140	6 AR086858	AR086858 Sequence
2	2137	99.9	2137	6 AR086871	AR086871 Sequence
3	2046	95.6	2039	6 AR086859	AR086859 Sequence
4	2043	95.5	2096	6 AR086872	AR086872 Sequence
5	2012.8	94.1	2145	8 CSNADP	X58832 C. sorokina
6	1969	92.0	1969	6 AR086860	AR086860 Sequence
7	1501.4	70.2	1506	6 AR086876	AR086876 Sequence
8	1470	68.7	1473	6 AR086877	AR086877 Sequence
9	592.2	27.7	10256	1 AE004872	AE004872 Pseudomonas
10	573.2	26.8	1628	1 PAE15166	Y15166 Pseudomonas
11	572.4	25.7	11163	1 AE014684	AE014684 Bifidobac
12	572.4	26.7	349980	6 AX492783	AX492783 Sequence
13	572.4	26.7	349980	6 AX533950	AX533950 Sequence
14	565.2	26.4	1628	1 PAE18494	Y18494 Pseudomonas
15	554.4	25.9	292100	1 SC0939121	AL939121 Streptomy
16	551.6	25.8	110000	1 AP006618	Continuation (48 o
17	551.6	25.8	9872	8 CGSDHANC	X58831 C. sorokina
18	548.6	25.6	1691	3 GIADADPDGH	M84604 Giardia lam
19	541	25.3	1113	3 AF533883	AF533883 Spironuc

20	532.4	24.9	346287	1 BX640450	BX640450 Bordetell
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22	529.2	24.7	348171	1 BX640412	BX640412 Bordetell
23	526	24.6	104170	2 AC091510	AC091510 Leishmani
24	523	24.4	10495	1 AE002013	AE002013 Deinococc
25	515.8	24.1	346259	1 BX640435	BX640435 Bordetell
26	514.6	24.0	1119	3 AF069057	AF069057 Giardia i
27	510.2	23.8	1123	3 AY178744	AY178744 Giardia i
28	508.4	23.8	1114	3 AY178742	AY178742 Giardia i
29	508.2	23.7	1121	3 AY178743	AY178743 Giardia i
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31	495	23.1	1114	3 AF060983	U60983 Giardia int
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40	487.6	22.8	1114	3 AY178747	AY178747 Giardia i
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42	487.2	22.8	1117	3 AY178746	AY178746 Giardia i
43	480.6	22.5	2653	1 XXGDH	X16399 Gene for g1
44	479.6	22.4	1094	3 GU60982	U60982 Giardia int
45	474.8	22.2	1443	1 AF321093	AF321093 Pseudomon

## ALIGNMENTS

RESULT 1	AR086858	Sequence 1 from patent US 5985634.	2140 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AR086858	Sequence 1 from patent US 5985634.				
DEFINITION	AR086858					
ACCESSION	AR086858					
VERSION	AR086858.1	GI:10013624				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 2140)					
AUTHORS	Schmidt, R.R. and Miller, P.					
TITLE	Polypeptides and polynucleotides relating to the alpha- and beta-subunits of glutamate dehydrogenases and methods of use					
JOURNAL	Patent: US 5985634-A 1 16-NOV-1999;					
FEATURES	Location/Qualifiers					
source	1..2140					
ORIGIN	1..2140					
ORIGIN	/organism="Unknown"					
ORIGIN	/mol_type="unassigned DNA"					
Query Match	100.0%; Score 2140; DB 6; Length 2140;					
Best Local Similarity	100.0%; Pred. No. 1.5e-242;					
Matches 2140; Conservative	0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1 CTCCTTCTGCTGCGCCCTCTCTCCGTCAGACAGACCGCCCTCGTCCGAAGCTTA	60				
QY	61 TCGGCG	120				
DB	61 TCGGCG	120				
QY	121 TCCGTCGCGCAAGGCGCATCTCCGCGCAAGGCGCGTCTCGTGGAGAGAGATCTCG	180				
DB	121 TCCGTCGCGCAAGGCGCATCTCCGCGCAAGGCGCGTCTCGTGGAGAGAGATCTCG	180				
QY	181 CGATGACGCCACCAACCGGCACTTACGCGCTGCGAGAGAGCGGTGAAGAGATGCGCA	240				
DB	181 CGATGACGCCACCAACCGGCACTTACGCGCTGCGAGAGAGCGGTGAAGAGATGCGCA	240				
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Db 301 TGACCGAATATCTTCAATGAAGACCCGAGCAGCAGAGATTCATGAGCGCGTGCAGG 360  
Oy 361 TGCGCGCTCTCCCTGAGCGCGCTGTTGAGAGCGCGCGAGCTGCTGCGCATCTTCAAGC 420  
Db 361 TGCGCGCTCTCCCTGAGCGCGCTGTTGAGAGCGCGCGAGCTGCTGCGCATCTTCAAGC 420  
Oy 421 AGATGTTGAGCTGAGCGCGCTGATCACTTTCCGCTGCTGCTGCTGAGCAAGCGCGCA 480  
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Oy 601 AGATCTTCAAGAACAGCTGACCACTGCTGCGCATGAGCGCGCGCAAGCGCGCTTCCG 660  
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Oy 961 AGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
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Db 1321 CTTCCACCAAGAGCGCATCCCAAGTACAAAGAGCGCGCATCTTATGCTGCGCGCA 1380

Db 1321 CTTCCACCAAGAGCGCATCCCAAGTACAAAGAGCGCGCATCTTATGCTGCGCGCA 1380  
Oy 1381 AGCGCGCGCAAGCGCGCGCTGAGCGCTGAGAGATGAGCGAGAGAGAGAGAGAGAG 1440  
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Db 1501 AGAAGTCCGCGCATGAGCGCGCTGAGCGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560  
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Oy 1801 CGGCTATTTTTCAGCGAGCGCGCTGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
Db 1801 CGGCTATTTTTCAGCGAGCGCGCTGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
Oy 1861 GCTGACGCTGCGCGCGAGCTTTCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
Db 1861 GCTGACGCTGCGCGCGAGCTTTCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
Oy 1921 CAGCTGTTGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
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Oy 1981 CCGCGAATTTTTCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040  
Db 1981 CCGCGAATTTTTCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040  
Oy 2041 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100  
Db 2041 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100  
Oy 2101 GTAAACAG 2140  
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RESULT 2  
AR086871  
LOCUS AR086871 2137 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 18 from patent US 5985634.  
ACCESSION AR086871  
VERSION AR086871.1 GI:10013637  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2137)  
AUTHORS Schmidt,R.R. and Miller,P.  
TITLES Polypeptides and polynucleotides relating to the .alpha.- and  
beta.-subunits of glutamate dehydrogenases and methods of use  
JOURNAL Patent: US 5985634-A 18 16-NOV-1999;  
FEATURES  
1..2137  
location/Qualifiers  
/organism="unknown"



[illegible]

D	b	559	AGATCTTCAAGAAACACCTGACACACCTGTCACATGGGCGCGGCAAGGGCGCGCTCCAGCT	618
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D	b	619	TCGACCCCAAGGGCAAGCGACCGGGAGGTATGCGCTTCTGCCAGTCTTCATGACCG	678
O	y	721	AGCTGACGGCCCAATCAGCTACGTGTGACGAGAGTGCCTGGCGGACATTCGGCGTGGCG	780
D	b	679	AGCTGACGGCCCAATCAGCTACGTGTGACGAGAGTGCCTGGCGGACATTCGGCGTGGCG	738
O	y	781	CGCGCGAGATTGACTACTTTTCGCGCAATACAGCGCATCAACAAGAACTACACCGCG	840
D	b	739	CGCGCGAGATTGACTACTTTTCGCGCAATACAGCGCATCAACAAGAACTACACCGCG	798
O	y	841	TGCTGACCCCGAAGGGCCAGAGAGTATGCGCGCTCCGAGATCCGCCCGAGGCCACCGCT	900
D	b	799	TGCTGACCCCGAAGGGCCAGAGAGTATGCGCGCTCCGAGATCCGCCCGAGGCCACCGCT	858
O	y	901	ACGCGCGCGCTGCTGTTTGTGTGAGAAACGTGTGAGAACAAAGGCGAGAGCCTCMAAGGCA	960
D	b	859	ACGCGCGCGCTGCTGTTTGTGTGAGAAACGTGTGAGAACAAAGGCGAGAGCCTCMAAGGCA	918
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D	b	979	AGAAAGGCGCCATGTGTGTGTGCTGTGCTGTCCGACTCCAGGGCTACGTGTACGAGCCCAAG	1038
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D	b	1039	GCTTCACGCGCCGAGACGTGTGACGGCGGTGCAAGACATGAAAGAAAGAACACACGCGC	1098
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D	b	1099	GCAATCTCGAGTACAAAGAGCGAACACCGCGGTGTATGTGTGCGACACCGCGCAAGCTTTGGG	1158
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D	b	1159	AGCTGACCTGCGCAGGTGTGACATTCGCTTCCCTGCGCCACCCAGAACGAGATCGATGAGC	1218
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D	b	1219	ACGACGCGCGAGCTGTGTGATCAGACACGCGTCCAGTACGTGTGTGAGGGCGCCACATGC	1278
O	y	1321	CCTCCACCAAGAGGGCCATCCACAATACAAAGGCGCGCATCATCTACTGCCCGGCA	1380
D	b	1279	CCTCCACCAAGAGGGCCATCCACAATACAAAGGCGCGCATCATCTACTGCCCGGCA	1338
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D	b	1339	AGGCGGCGCAACGCGCGCGCGGTGTGCGCGGTACGCGCGCTGTGAGATGACCCAGAACCGCATGA	1398
O	y	1441	GCGTGAACGTGAACTCGGAGAGAGTTTCGGACAAAGCTGGAAGGCATCATGAAAGACATCT	1500
D	b	1399	GCGTGAACGTGAACTCGGAGAGAGTTTCGGACAAAGCTGGAAGGCATCATGAAAGACATCT	1458
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D	b	1459	ACGACCTCCGCGCATGGGGCGTCCCGAGATACAAATTTGACCTGGCTGCGGGCGCCAAACA	1518
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QY	1741	GCGCCGAGCCCCCTGCATTTCAACCCGAAGAATCTAGCGGCAATTGACTGCATCAGAGA	1800
Db	1699	GCCCCGTGCCCTTCGCAATTTCAACCCGAAGAATCTAGCGGCAATTGACTGCATCAGAGA	1756
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QY	1921	CACCCTGTTGGAAGCCACAGAGCTCAATTGCGCTTTTAGTGAATGTGAGCCCCCTCCAGC	1980
Db	1879	CACCCTGTTGGAAGCCACAGAGCTCAATTGCGCTTTTAGTGAATGTGAGCCCCCTCCAGC	1938
QY	1981	CCCCGAATTTTCTTGCCATGAGACGTGCGGTTCTTAGCGCTGTGTGACCCCAAATGACAGTT	2040
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QY	2041	AGTGTGCGTGCTTGCCCTGCGCTGACCCGGGATGCGATACGTGACTCTGAAGTGTCTTGT	2100
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Db	2059	GTAATAACGACGAGTCMAAAAAAAAAAAAAAAAAAAAAA	2098

RESULT 4			
AR086872			
LOCUS	AR086872	2096 bp	DNA
DEFINITION	Sequence 19 from patent US 5965654.		linear
			PAT 07-SEP-2000

SOURCE	Unknown.
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Unclassified.

**AUTHORS** Schmidt, R.R. and Miller, P.

.beta.-subunits of glutamate dehydrogenases and methods of use

## FEATURES

### Location/Qualifiers

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/organism="unknown"
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## ORIGIN

Query Match	95.5%	Score 2043;	DB 6;	Length 2096;
Best Local Similarity	98.0%	Pred. No. 3.8e-231;		
Matches 2095;	Conservative 0;	Mismatches 0;	Indels 42;	Gaps 1;

QY	4	CTTTCTGTGCGCCCTCTCTCGCTCCGCGCAGAGACCGCCCTGTGCGCAAGCCTATACG	63
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QY	64	TGCGCGCGCCCGCTGTGCGGACGCCCGCGCTGTGCGCCGTCGCGCGTGTGCGGTGCGGTTC	123
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QY	124	GCTTCGCGCAAGCGCGATGTCCGCGCGCAAGGCGGTCTCGCTGAGAGAGCAGATCTTCCGCGA	183
Db	79	GCTTCGCGCAAGCGCGATGTCCGCGCGCAAGGCGGTCTCGCTGAGAGAGCAGATCTTCCGCGA	138
QY	184	TGAGCGGACCAACCGGCGGACTTTCAACGGGCGTGCAGAAAGCGGTGAGACGAGATGGCGACCA	243
Db	139	TGAGCGGACCAACCGGCGGACTTTCAACGGGCGTGCAGAAAGCGGTGAGACGAGATGGCGACCA	198
QY	244	AGGCGGGGACTGAGGGGCTGTGTGACGGGCACTCAGATCCCGACGTGTGCGGCGAAGCTGTCTGA	303

Db	199	AGGGGGGACATGAGGGGCTTGATGACGGGCATCAAGAAACCCCGACGTGCGCAGCTGTGA	258
Qy	304	CCGAGATCTTCATGTAAGACCCCGAGACGACGAGTTCAATGCAAGCGGTGGCGAGGTGG	363
Db	259	CCGAGATCTTCATGTAAGACCCCGAGACGACGAGTTCAATGCAAGCGGTGGCGAGGTGG	318
Qy	364	CCGCTCTCCCTGACAGCCCGTGTTCAGAAAGCGCCCGAGCTGCTCCCATCTTCAAGCAGA	423
Db	319	CCGCTCTCCCTGACAGCCCGTGTTCAGAAAGCGCCCGAGCTGCTCCCATCTTCAAGCAGA	378
Qy	424	TCGTTGAGCCTGAGCGCGTGTATCACTTTCGCGGTCTGTGCTGTGGAACGCGCGGCAAC	483
Db	379	TCGTTGAGCCTGAGCGCGTGTATCACTTTCGCGGTCTGTGCTGTGGAACGCGCGGCAAC	438
Qy	484	TGCAAGTCAACCCGGGCTTCCGGGTGCAATCTGTCCGCATGTGGCCCTTCAAGGGCG	543
Db	439	TGCAAGTCAACCCGGGCTTCCGGGTGCAATCTGTCCGCATGTGGCCCTTCAAGGGCG	498
Qy	544	GCCGAGCCTTCAACCCCGGTGAACTGTTCATCATGAAGTTCTTGGCCTTGAAGCAGA	603
Db	499	GCCGAGCCTTCAACCCCGGTGAACTGTTCATCATGAAGTTCTTGGCCTTGAAGCAGA	558
Qy	604	TCTTCAAGAAACAGCTTACCACTTGGCCCATATGGCGCGCGACAGGGCGGCTCCGACTTGC	663
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Qy	664	ACCCCAAGGGCAAGGCGACGCGGGAGTGTATGCTTCTGCACTCTTCAATGACCGAGC	723
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Qy	724	TGCAAGGSCCATCTAGCTACGTGCAAGGACGTGCGCGCGCGGACATGGCGGTGGCGCG	783
Db	679	TGCAAGGSCCATCTAGCTACGTGCAAGGACGTGCGCGCGCGGACATGGCGGTGGCGCG	738
Qy	784	GCGAGATTGGCTACTCTTTGCGCCAGTACAAGCGCATCAACAAGACTTCAACCGCGTGC	843
Db	739	GCGAGATTGGCTACTCTTTGCGCCAGTACAAGCGCATCAACAAGACTTCAACCGCGTGC	798
Qy	844	TGACCCCGAAAGGGCCAGAGATATGGCGGCTTCCAGATCCGCGCCGAGGCCACCGGCTACG	903
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Db	859	GCGCGGTGCTGTTTGTGGAACGTGCTGAAGGACAAAGGCGGAGAGCTTCAAGGGCAAGC	918
Qy	964	GCTGCGGTGCTGCTGGCGCGGGGCAACGTGGCCAGTACTGGCGGAGAGCTGCTGTGAGGA	1023
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Qy	1024	AGGGCGCCATCTGATGCTGCTGCTGCTGCATCTCCAGGGCTACGTGTACGAGCCCAACGGCT	1083
Db	979	AGGGCGCCATCTGATGCTGCTGCTGCTGCATCTCCAGGGCTACGTGTACGAGCCCAACGGCT	1038
Qy	1084	TCACGCGCGAGCACTTCAGAGCGGTGCAAGCATGAAGAAAGAACACACGCGCCGCA	1143
Db	1039	TCACGCGCGAGCACTTCAGAGCGGTGCAAGCATGAAGAAAGAACACACGCGCCGCA	1098
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Qy	1264	ACGCGAGCTGCTGATCAAGACAGGCTGCGCAATCTGTGTGAAGAGCGGCCCACTGCTCT	1323
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DB 2059 AACACGAGAGTCAAAAAA 2095

RESULT 5  
CSNADP 2145 bp mRNA linear PLN 29-MAY-1992  
LOCUS C.sorokiniana NADP-gdh mRNA for NADP-specific glutamate  
DEFINITION hydroxymethylglutamate.  
ACCESSION X58832  
VERSION X58832.1 GI:18272  
KEYWORDS NADP-gdh gene; NADP-specific glutamate dehydrogenase.  
SOURCE Chlorella sorokiniana  
ORGANISM Chlorella sorokiniana  
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae;  
Chlorellales; Chlorellaceae; Chlorella.

REFERENCE  
AUTHORS Cook,J.M., Kilm,K.D., Miller,P.W., Hutson,R.G. and Schmidt,R.R.  
TITLE A nuclear gene with many introns encoding ammonium-inducible  
chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella  
sorokiniana  
JOURNAL Plant Mol. Biol. 17 (5), 1023-1044 (1991)  
MEDLINE 92032762

PUBMED 1718478  
REFERENCE 2 (bases 1 to 2145)  
AUTHORS Schmidt,R.R.  
TITLE Direct Submission  
JOURNAL Submitted (03-APR-1991) R.R. Schmidt, University of Florida, Dept  
of Microbiology and Cell Biology, 3103 McCarty Hall, Gainesville FL  
32611, USA  
COMMENT See X58831 for related sequence  
ATTENTION: X5881 and X5882 were incorrectly reported as having  
one accession number (X58832) in the reference [2].  
FEATURES  
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Query Match 94.1%; Score 2012.8; DB 8; Length 2145;  
Best Local Similarity 98.5%; Pred. No. 1.3e-227;  
Matches 2076; Conservative 0; Mismatches 22; Indels 10; Gaps 4;  
QY 34 TGACAGACGCGCTGTCGCGCAAGCTATGTCGCGCGCGCTGCGCGCAAGCGCGCGCT 93  
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QY 213 CTGAGAGAGCGGAGAGAGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 272  
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RESULT 6  
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LOCUS AR086860 1969 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 7 from patent US 5985634.  
ACCESSION AR086860  
VERSION AR086860.1 GI:10013626  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 1969)  
AUTHORS Schmidt,R.R. and Miller,P.  
TITLE Polypeptides and polynucleotides relating to the .alpha.- and .beta.-subunits of glutamate dehydrogenases and methods of use  
JOURNAL Patent: US 5985634-A 7 16-NOV-1999;  
FEATURES  
Location/Qualifiers  
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ORIGIN  
Query Match 92.0%; Score 1969; DB 6; Length 1969;  
Best Local Similarity 100.0%; Pred. No. 1.9e-222;  
Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



TITLE Polypeptides and polynucleotides relating to the .alpha.- and .beta.-subunits of glutamate dehydrogenases and methods of use  
JOURNAL Patent: US 5985634-A 23 16-NOV-1999;  
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DEFINITION Sequence 25 from patent US 5985634.  
ACCESSION AR086877  
VERSION AR086877.1 GI:10013643  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1473)  
AUTHORS Schmidt,R.R. and Miller,P.  
TITLE Polypeptides and polynucleotides relating to the .alpha.- and .beta.-subunits of glutamate dehydrogenases and methods of use  
JOURNAL Patent: US 5985634-A 25 16-NOV-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 9e-164;  
Matches 1470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE  
 AUTHORS  
 1 (bases 1 to 10256)  
 Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltzy, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.U., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T.  
 Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
 TITLE  
 JOURNAL NATURE 406 (6799), 959-964 (2000)  
 MEDLINE 20437337  
 PUBMED 10984043

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 AUTHORS  
 2 (bases 1 to 10256)  
 Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltzy, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.U., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reiter, J., Sater, M.H., Hancock, R.E.W., Lory, S., and Olson, M.V.  
 Direct Submission  
 TITLE  
 JOURNAL Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA  
 MEDLINE 3 (bases 1 to 10256)

REFERENCE  
 AUTHORS  
 Pseudomonas aeruginosa Community Annotation Project (PseudocAP)  
 TITLE  
 JOURNAL Direct Submission  
 JOURNAL Submitted (04-FEB-2003) Department of Molecular Biology and Biochemistry, Simon Fraser University, 8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada

COMMENT  
 This represents the February 3, 2003 version of the continually updated, reviewed, *Pseudomonas aeruginosa* PA01 genome annotation, from PseudocAP (see <http://www.pseudomonas.com> for latest updates and links to alternate annotations). PseudocAP is coordinated by



Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert B.W. Hancock (University of British Columbia, Canada). We welcome submission through [www.pseudomonas.com](http://www.pseudomonas.com) of any proposed changes.

'Protein name confidence' is used to rate our confidence of the accuracy of the protein name.

Class 1: Function experimentally demonstrated in *P. aeruginosa*.

Class 2: Function of highly similar gene experimentally demonstrated in another organism (and gene context consistent in terms of pathways its involved in, if known).

Class 3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene.

Class 4: Homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences.

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Pseudomonas aeruginosa  
gdhA gene; NADP-glutamate dehydrogenase.  
Pseudomonas aeruginosa  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.

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JOURNAL

Submitted (21-OCT-1997) P. R. Brown, Kings College London, Molecular  
Biology and Biophysics Group, Strand, London, WC2R 2LS, UK  
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FEATURES  
source  
gene  
CDS

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Pseudomonas aeruginosa gdhA gene, strain PAO1.  
Pseudomonas aeruginosa  
gdhA gene; NADP-glutamate dehydrogenase.  
Pseudomonas aeruginosa  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.

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11163 bp DNA linear BCT 15-AUG-2003  
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 AE014684 AE014295  
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Bifidobacterium longum NCC2705  
 Bifidobacterium longum NCC2705  
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 1 (bases 1 to 11163)  
 Schell, M.A., Karmirantzou, M., Snel, B., Vilanova, D., Berger, B.,  
 Pessi, G., Zwielen, M.-C., Desiere, F., Bork, P., Delley, M.,  
 Pridmore, D. and Arigoni, F.  
 The genome sequence of Bifidobacterium longum reflects its  
 adaptation to the human gastrointestinal tract  
 Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14422-14427 (2002)  
 12381787  
 2 (bases 1 to 11163)  
 Schell, M.A., Karmirantzou, M., Snel, B., Vilanova, D., Berger, B.,  
 Pessi, G., Zwielen, M.-C., Desiere, F., Bork, P., Delley, M.,  
 Pridmore, D. and Arigoni, F.  
 Direct Submission  
 Submitted (27-AUG-2002) Bioscience Resource Project, P.O.  
 Box 44, Lausanne 26 1000, Switzerland  
 location/Qualifiers

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Query Match 26.7%; Score 572.4; DB 1; Length 11163;

Best Local Similarity 66.9%; Pred. No. 1.7e-58;

Matches 886; Conservative 0; Mismatches 411; Indels 27; Gaps 4;

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## RESULT 12

AX492783 349980 bp DNA linear PAT 26-SEP-2002

LOCUS Sequence 1101 from Patent EP1227152.

ACCESSION AX492783

VERSION AX492783.1 GI:23338466

## KEYWORDS

SOURCE Bifidobacterium longum biovar Longum

ORGANISM Bifidobacterium longum biovar Longum

REFERENCE 1 Bacteria; Actinobacteria; Actinobacteriales; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium.

AUTHORS None.

TITLE Bacterial strain and genome of Bifidobacterium

JOURNAL Patent: EP 1227152-A 1101 31-JUL-2002;

FEATURES location/Qualifiers

1. 349980

2. 156638

3. 156638

4. 156638

5. 156638

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11. 156638

12. 156638

## ORIGIN

Query Match 26.7%; Score 572.4; DB 6; Length 349980;  
Best Local Similarity 66.9%; Pred. No. 8.1e-59;  
Matches 886; Conservative 0; Mismatches 411; Indels 27; Gaps 4;

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ACCESSION AX553950
VERSION AX553950.1 GI:25897903
KEYWORDS
SOURCE
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Bifidobacterium longum biovar Longum
Bacteria; Actinobacteria; Actinobacteriales;
Bifidobacteriaceae; Bifidobacterium.

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REFERENCE
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AUTHORS Arigoni, F., Delley, M., Mollet, B., Fridmore, R.D., Schell, M.A.,
Pohl, T.G., and Zwielen, M.C.
TITLE The genome of a bifidobacterium
JOURNAL Patent: WO 02074798-A 4 26-SEP-2002;
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Query Match 26.7%; Score 572.4; DB 6; Length 349980;
Best Local Similarity 66.9%; Pred. No. 8,1e-59;
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 ORGANISM Streptomyces coelicolor A3(2)  
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 Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)  
 Nature 417 (6885), 141-147 (2002)  
 JOURNAL MEDLINE 21996410  
 PUBMED 12000953  
 REFERENCE 2 (bases 1 to 292100)  
 AUTHORS Bentley, S.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces Sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: sdb@sanger.ac.uk  
 COMMENT On or before Oct 30, 2002 this sequence version replaced gi:3449234, gi:7288050, gi:7320887, gi:7321265, gi:7649562, gi:8218190, gi:9367445, gi:11544744, gi:20520684.  
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SCD40A.01, rpoC, DNA-directed RNA polymerase beta' chain (fragment), len: >279 aa: similar to C-terminal region of SW:RPOC_BACSU (EMBL:L43593) Bacillus subtilis DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) RpoC, 1199 aa; fasta scores: opt: 801 z-score: 911.4 E(): 0; 53.0% identity in 247 aa overlap"
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Db 34099 GCGAAGCAGACGCGATCTCAACCTTCACACCTCTTACCGAGATCGAGTGGCAACC 34158
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Dh 35407 CGAGCGGTGGCGGAGCGGATGCTGGCGGAGGGGTGATCTGACGAGACC 35456

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 9, 2005, 17:34:32 ; Search time 1075 Seconds  
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11784.415 Million cell updates/sec

Title: US-10-627-886-1  
Perfect score: 2140  
Sequence: 1 CTCCTTCTGCTGCGCCCTCT.....AAAAAAAAAAAAAAAAAAAA 2140

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: geneSeqn2002bs:\*  
7: geneSeqn2002bs:\*  
8: geneSeqn2003as:\*  
9: geneSeqn2003bs:\*  
10: geneSeqn2003cs:\*  
11: geneSeqn2003ds:\*  
12: geneSeqn2004as:\*  
13: geneSeqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2140	100.0	2140	2	AAT64529
2	2140	100.0	2140	6	ABK51007
3	2137	99.9	2137	2	AAT64542
4	2137	99.9	2137	6	ABK51020
5	2046	95.6	2099	2	AAT64530
6	2046	95.6	2099	6	ABK51008
7	2043	95.5	2096	2	AAT64543
8	2043	95.5	2096	6	ABK51021
9	2040	95.3	2124	12	ADQ36706
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11	1969	92.0	1969	6	ABK51009
12	1935.8	90.5	2083	12	ADQ36708
13	1691	79.0	2084	12	ADQ36723
14	1611	75.3	2045	12	ADQ36724
15	1565	73.1	1922	12	ADQ36712
16	1501.4	70.2	1506	6	ABK51025
17	1499.8	70.1	1506	2	AAT64547
18	1489.8	69.6	1505	12	ADQ36728
19	1470	68.7	1473	2	AAT64548
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21	1470	68.7	1473	12	ADQ36730	Adq36730 Mature NA
22	592.2	27.7	1497	11	ABD05527	Abd05527 Pseudomon
23	590.8	27.6	1338	8	ACA42633	ACA42633 Prokaryot
24	590.8	27.6	1333	11	ABD05471	ABD05471 Pseudomon
25	572.4	26.7	349980	6	ABQ81845	Abq81845 Bifidobac
26	529.2	24.7	1392	8	ACA27224	ACA27224 Prokaryot
27	526.2	24.6	1347	8	ACA43484	ACA43484 Prokaryot
28	508.2	23.7	1275	13	AD545874	Ad545874 Bacterial
29	500.4	23.4	1314	13	AD558634	Ad558634 Bacterial
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31	489.8	22.9	1344	5	AAF87487	AAF87487 Corynebact
32	488.6	22.8	1332	8	ACA41075	ACA41075 Prokaryot
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34	472.6	22.1	1332	6	AA597271	AA597271 Neisseria
35	472.6	22.1	1335	8	ACA41987	ACA41987 Prokaryot
36	469.2	21.9	1242	10	AB238921	Ab238921 N. gonorr
37	467.6	21.9	35133	3	AAA81518	AAA81518 N. mening
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39	467.6	21.9	349980	3	AAF21611	AAF21611 Neisseria
40	460.8	21.5	1344	13	AD556228	Ad556228 Bacterial
41	451.6	21.1	1359	11	ACH94971	Ach94971 Klebsiell
42	447	20.9	1341	8	ACA36189	ACA36189 Prokaryot
43	436	20.4	1344	5	AAF87488	AAF87488 Brevibact
44	435.8	20.4	349980	5	AAH68531	AAH68531 C. glutami
45	435.6	20.4	2190	2	AAQ37237	Aaq37237 gdhA gene

## ALIGNMENTS

RESULT 1	
ID	AAT64529 standard; CDNA; 2140 BP.
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XX	AAT64529;
XX	
DT	17-OCT-2003 (revised)
DT	10-JUL-1997 (first entry)
XX	
DE	NADP-specific glutamate dehydrogenase alpha-subunit precursor CDNA.
XX	
XX	Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW	chloroplast; transgenic plant; ds.
XX	
OS	Chlorella sorokiniana; strain UTEX 1230.
XX	
XX	
FT	Key location/Qualifiers
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FT	transit_peptide 33..152 /*tag= b
FT	mat_peptide 153..1610 /*tag= c
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PD	10-APR-1997.
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XX	03-OCT-1996; 96WO-US015921.
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XX	06-OCT-1995; 95US-00541033.
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XX	(UYFL ) UNIV FLORIDA.
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PI	Schmidt RR, Miller P;
XX	
DR	WPI: 1997-226226/20.
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XX	P-PSDB; AAW15407.
XX	
PT	DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT	sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT	plant cells.
XX	

PS Claim 2; Page 25-27; 61bp; English.

CC cDNA clones (AA154529 and AA154530) respectively code for the alpha  
CC subunit (AA154507) and beta subunit (AA154508) precursor proteins of an  
CC ammonium-inducible, chloroplast-localised NADP-specific glutamate  
CC dehydrogenase (NADP-GDH) of *Chlorella sorokiniana*. They have been  
CC deposited in E. coli DH5alpha as ATCC 69925 and ATCC 69926, respectively.  
CC The precursor proteins are processed to yield mature alpha and beta  
CC subunits (see also AA154547-48) that comprise the active NADP-GDH  
CC hexameric isoenzymes. The nitrogen metabolism of plants can be modulated  
CC (pref. increasing the assimilation of inorganic N into organic N) by  
CC transforming them with nucleotide sequences encoding the alpha and/or  
CC beta subunits. Such plants show improved properties, e.g. increased crop  
CC yield and improved stress tolerance. Heterohexamers having alpha and beta  
CC subunits can be expressed that have higher aminating/deaminating activity  
CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.  
CC (Updated on 17-OCT-2003 to standardise OS field)

CC XX Sequence 2140 BP; 416 A; 734 C; 632 G; 358 T; 0 U; 0 Other;

Query Match 100.0%; Score 2140; DB 2; Length 2140;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCTTTCTGCTGCGCTCTCTCTCCGTCATGCAAGCCCTCTGCGCAAGCTTA 60  
DB 1 CTCTTTCTGCTGCGCTCTCTCTCCGTCATGCAAGCCCTCTGCGCAAGCTTA 60  
QY 61 TGTGTGCG 120  
DB 61 TGTGTGCG 120  
QY 121 TCCGCTCCGCGCAAGCGCGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 121 TCCGCTCCGCGCAAGCGCGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
QY 181 CGATGAGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
DB 181 CGATGAGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
QY 241 CCAAGCG 300  
DB 241 CCAAGCG 300  
QY 301 TGACCGAGATCTTCAAGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
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DB 361 TGGCGCTCTCCGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
QY 421 AGATGTTGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
DB 421 AGATGTTGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
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QY 1681 CGGAAAGGCGCGCTTTTCCAGCGAGGCGCGCGCGCGCGCGCGCGCGCG 1740  
DB 1681 CGGAAAGGCGCGCTTTTCCAGCGAGGCGCGCGCGCGCGCGCGCGCGCG 1740  
QY 1741 GCGCGCGTGCCTGCAATTCACCCCAAGAAAGTGAAGGCGCGCGCGCGCG 1800  
DB 1741 GCGCGCGTGCCTGCAATTCACCCCAAGAAAGTGAAGGCGCGCGCGCGCG 1800  
QY 1801 CGGCTATTTTTCGCGACGCGCGCTCACCGAGAGCTCTCTCCCGAGCGCT 1860  
DB 1801 CGGCTATTTTTCGCGACGCGCGCTCACCGAGAGCTCTCTCCCGAGCGCT 1860



Db 1801 CGGCTATTTTTCGCGACGCGGCTCAACCCGAGAGCTCTCTCCCGGAGCCCTTAAGC 1860  
 QY 1861 GGTGACGTCGCGCCGACCTTGGCTGCGACATGCTGCTTGAACCCCTCGAGTCAAC 1920  
 Db 1861 GGTGACGTCGCGCCGACCTTGGCTGCGACATGCTGCTTGAACCCCTCGAGTCAAC 1920  
 QY 1921 CACCTGTGTGAGAGCTACGAGCTCAATTGCTTTTATGTATGTATGCGCCCTCTGTC 1980  
 Db 1921 CACCTGTGTGAGAGCTACGAGCTCAATTGCTTTTATGTATGTATGCGCCCTCTGTC 1980  
 QY 1991 CCGGCAATTTTCTGTCATGAGAGCTGCGGTTCTTAGCCTGTGACCCCAAGTACGATT 2040  
 Db 1991 CCGGCAATTTTCTGTCATGAGAGCTGCGGTTCTTAGCCTGTGACCCCAAGTACGATT 2040  
 QY 2041 AGTGTGCGGCTTCCGCTGCGCTGCGCGGATGCGATCTGTGACCTGTGAGAGTCTTGT 2100  
 Db 2041 AGTGTGCGGCTTCCGCTGCGCTGCGCGGATGCGATCTGTGACCTGTGAGAGTCTTGT 2100  
 QY 2101 GTTAAACAGCAGAGTCAAAAAA 2140  
 Db 2101 GTTAAACAGCAGAGTCAAAAAA 2140

## RESULT 2

ABKS1007 standard; cDNA; 2140 BP.

ABKS1007;

24-SEP-2002 (first entry)

cDNA encoding NADP-glutamate dehydrogenase alpha subunit.

NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;  
 nitrogen metabolism; plant; ammonium assimilation; transgenic;  
 ammonia toxicity tolerance; osmotic stress tolerance; gene; ss.

Chlorella sorokiniana.

Key Location/Qualifiers  
 CDS 33..1613  
 FT /\*tag= a  
 FT /product= "NADP-specific glutamate dehydrogenase alpha  
 subunit"

US2002062495-A1.

23-MAY-2002.

01-MAY-1998; 98US-00070844.

01-MAY-1998; 98US-00070844.

(SCHMIDT R R.

(MILLER) MILLER P.

Schmidt RR, Miller P;

WPI; 2002-499691/53.

P-PSDB; AAU98950.

Transforming a plant with a polynucleotide encoding a polypeptide with  
 glutamate dehydrogenase activity provides a plant with modulated nitrogen  
 metabolism useful to increase yield and ammonium and osmotic stress  
 tolerance.

Disclosure; Page 11-13; 35pp; English.

The invention relates to a method of modulating nitrogen metabolism in  
 plant cells, comprising transforming a plant cell with a polynucleotide  
 encoding a polypeptide having glutamate dehydrogenase activity, and  
 culturing the cell to produce descendant cells which express the  
 polypeptide. The method is used to provide plants with increased yield.

CC Improved ammonium assimilation properties, increased tolerance to ammonia  
 toxicity, improved osmotic stress tolerance and improved composition. The  
 CC present sequence represents the coding sequence of Chlorella sorokiniana  
 CC NADP-glutamate dehydrogenase alpha subunit, used in the method of the  
 CC invention

SQ Sequence 2140 BP; 416 A; 734 C; 632 G; 358 T; 0 U; 0 Other;

Query Match 100.0%; Score 2140; DB 6; Length 2140;

Beet Local Similarity 100.0%; Pred. No. 0;

Matches 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTTGCTCGCCCTCTCTCGTCCGCGATGACAGCCGCTCTCCCAAGCTTA 60  
 Db 1 CTCCTTTGCTCGCCCTCTCTCGTCCGCGATGACAGCCGCTCTCCCAAGCTTA 60  
 QY 61 TGTGACGCGCCCGCTGCGGACGCGCGCTGCTTGGCGCTGCGCTGCGG 120  
 Db 61 TGTGACGCGCCCGCTGCGGACGCGCGCTGCTTGGCGCTGCGCTGCGG 120  
 QY 121 TCCGCTCCGCGCAAGCGCATGCTCCGCGCAAGCGCGCTGCTGCGGAGAGATCTCG 180  
 Db 121 TCCGCTCCGCGCAAGCGCATGCTCCGCGCAAGCGCGCTGCTGCGGAGAGATCTCG 180  
 QY 181 CGATGACGCGCCACCGCGACTTCAAGCGCGCTGCAAGAGCGGTGAAGCATGCGCA 240  
 Db 181 CGATGACGCGCCACCGCGACTTCAAGCGCGCTGCAAGAGCGGTGAAGCATGCGCA 240  
 QY 241 CCAAGCGCGGACCTGAGGCGCTGCTGCAAGCGCGCATCAAGACCCGACGCTGCG 300  
 Db 241 CCAAGCGCGGACCTGAGGCGCTGCTGCAAGCGCGCATCAAGACCCGACGCTGCG 300  
 QY 301 TGACCGAGATCTTCAATGAAGACCCGAGCGAGCATGATGACAGCGGTGCGCGAG 360  
 Db 301 TGACCGAGATCTTCAATGAAGACCCGAGCGAGCATGATGACAGCGGTGCGCGAG 360  
 QY 361 TGGCGGTCTCCCTGAGCGCGCTGCTGCAAGCGCGCGAGCTGCTGCGCATCTTCAAGC 420  
 Db 361 TGGCGGTCTCCCTGAGCGCGCTGCTGCAAGCGCGCGAGCTGCTGCGCATCTTCAAGC 420  
 QY 421 AGATGTTGAGCTGAGCGCGCTGATCACTTCCGCGTGTCTGCTGCGAGCAAGCGCGCA 480  
 Db 421 AGATGTTGAGCTGAGCGCGCTGATCACTTCCGCGTGTCTGCTGCGAGCAAGCGCGCA 480  
 QY 481 ACCTGCAAGTCAACCGCGGCTTCCGCTGCGAGTACTGTCGCGCATCGGCCCTTCAAG 540  
 Db 481 ACCTGCAAGTCAACCGCGGCTTCCGCTGCGAGTACTGTCGCGCATCGGCCCTTCAAG 540  
 QY 541 GCGGCTGCGGCTTCCGCGGCTTCCGCGGAGCGCGTCAATGATGATGATGATGATGATG 600  
 Db 541 GCGGCTGCGGCTTCCGCGGCTTCCGCGGAGCGCGTCAATGATGATGATGATGATG 600  
 QY 601 AGATCTTCAAGACAGCTGAGCAACCTGCGCATGAGCGCGGAGCGCGCTTCCGACT 660  
 Db 601 AGATCTTCAAGACAGCTGAGCAACCTGCGCATGAGCGCGGAGCGCGCTTCCGACT 660  
 QY 661 TCGACCCCAAGGCGCAAGCGCAAGCGGAGTGTGCTTCTGCGCATGATGATGATG 720  
 Db 661 TCGACCCCAAGGCGCAAGCGCAAGCGGAGTGTGCTTCTGCGCATGATGATGATG 720  
 QY 721 AGCTGACGCGGCATCATGAGTGAAGCGAGCGTGGCGCGGAGCAATGCGCGGAGCG 780  
 Db 721 AGCTGACGCGGCATCATGAGTGAAGCGAGCGTGGCGCGGAGCAATGCGCGGAGCG 780  
 QY 781 CCGCGGAGATTTGGCTACTTTTCCGCGAGTCAAGCGCATCAAGAACTTCAACCGCG 840  
 Db 781 CCGCGGAGATTTGGCTACTTTTCCGCGAGTCAAGCGCATCAAGAACTTCAACCGCG 840  
 QY 841 TGTGACCCCGAAGGCGCGAGATGATGCGGCTCGAGATCGCGCGAGCGCGCGCT 900  
 Db 841 TGTGACCCCGAAGGCGCGAGATGATGCGGCTCGAGATCGCGCGAGCGCGCGCT 900  
 QY 901 ACGGCGCGTGTCTGTTGTGAGAAAGTGTGAAGCAAGCGGAGAGCTTCAAGGCA 960

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Db 901 ACGGCGCGTGCTGTTTGTGGAGACGTGCTGAAGACAAAGGCGAGCGCTCAAGGCGCA 960
Qy 961 AGCGTGCTGCTGTGCTGTCGCGCGGCGGACACGTGCGCCAGTATCGCGCGGAGCTGCTGTGG 1020
Db 961 AGCGTGCTGCTGTGCTGTCGCGCGGCGGACACGTGCGCCAGTATCGCGCGGAGCTGCTGTGG 1020
Qy 1021 AGAAGGCGCGCATGCTGCTGTGCTGTCGCGCTCCAGAGGCTACGTGTACGAGGCCAACG 1080
Db 1021 AGAAGGCGCGCATGCTGCTGTGCTGTCGCGCTCCAGAGGCTACGTGTACGAGGCCAACG 1080
Qy 1081 GCTTCACGCGCGAGAGCTGACAGGCGGTGCAGAGCATGAAAGAAACAACAAGCGGCC 1140
Db 1081 GCTTCACGCGCGAGAGCTGACAGGCGGTGCAGAGCATGAAAGAAACAACAAGCGGCC 1140
Qy 1141 GCATCTCCGAGTACAAAGACCAACCGCGGTGTATGTGGGCGACCGCGCGCAAGCTTGGG 1200
Db 1141 GCATCTCCGAGTACAAAGACCAACCGCGGTGTATGTGGGCGACCGCGCGCAAGCTTGGG 1200
Qy 1201 AGCTGAGCTGCGAGGTGAGCATCGCTTCCCTGCGCGCACCGAAGACGATCGATGAGC 1260
Db 1201 AGCTGAGCTGCGAGGTGAGCATCGCTTCCCTGCGCGCACCGAAGACGATCGATGAGC 1260
Qy 1261 ACGACGCGGAGCTGCTGATCAAGACAGCGGCTGCAGTACGTGGTGAAGGCGCGCAATGC 1320
Db 1261 ACGACGCGGAGCTGCTGATCAAGACAGCGGCTGCAGTACGTGGTGAAGGCGCGCAATGC 1320
Qy 1321 CCTCCACCAAGAGGCGCATCCACAGTACACAAAGCGCGCATCTACTACTGCCCCGCGCA 1380
Db 1321 CCTCCACCAAGAGGCGCATCCACAGTACACAAAGCGCGCATCTACTACTGCCCCGCGCA 1380
Qy 1381 AGGCGGCGCAAGCGCGCGCGGTGCGGTACAGCGGCGCTGGAAGTGAAGCCAGAACGCGATGA 1440
Db 1381 AGGCGGCGCAAGCGCGCGCGGTGCGGTACAGCGGCGCTGGAAGTGAAGCCAGAACGCGATGA 1440
Qy 1441 GCCTGAACGTGACCTGCGCAGAGAGGTTTCGCGACAAAGCTGGAAGCGCATCAATGAAGACATCT 1500
Db 1441 GCCTGAACGTGACCTGCGCAGAGAGGTTTCGCGACAAAGCTGGAAGCGCATCAATGAAGACATCT 1500
Qy 1501 ACGACTCCGCGCATGCGGCGCGTCCCGCAGATACATGTTGACTGTGCTGCGCGCGCAACA 1560
Db 1501 ACGACTCCGCGCATGCGGCGCGTCCCGCAGATACATGTTGACTGTGCTGCGCGCGCAACA 1560
Qy 1561 TCGCGGCGCTTCAACAAGGTGCTGATGCGGTCAAGGCGCCAGGCGCTGTTTAAGCTGCGC 1620
Db 1561 TCGCGGCGCTTCAACAAGGTGCTGATGCGGTCAAGGCGCCAGGCGCTGTTTAAGCTGCGC 1620
Qy 1621 AGGCGCAAGCGACGCGCTCAACCGGCAATCAACCAACCAACTCAACGCGCGCAAGACCTTTT 1680
Db 1621 AGGCGCAAGCGACGCGCTCAACCGGCAATCAACCAACCAACTCAACGCGCGCAAGACCTTTT 1680
Qy 1681 CGGAAAGCGGCGCTTTTCCAGCGAGGCGCTCACTGCGCTTCAATACCTGCTACTTT 1740
Db 1681 CGGAAAGCGGCGCTTTTCCAGCGAGGCGCTCACTGCGCTTCAATACCTGCTACTTT 1740
Qy 1741 GCGCGCGTGGCCCTGCAATTCACCCCAAGAAAGAACTAGCGGCACTTGAATGTCATCAGAGA 1800
Db 1741 GCGCGCGTGGCCCTGCAATTCACCCCAAGAAAGAACTAGCGGCACTTGAATGTCATCAGAGA 1800
Qy 1801 CGGCTATTTTTCGCGACGCGCGCTCAACCGGAGGCTCTTCCCGCGAGCCCTTAAGC 1860
Db 1801 CGGCTATTTTTCGCGACGCGCGCTCAACCGGAGGCTCTTCCCGCGAGCCCTTAAGC 1860
Qy 1861 GCTGACGTCGCGCGCACTTGTGCTGCGACATGCTGCTGTTTGAACCCCTCCAGCTACG 1920
Db 1861 GCTGACGTCGCGCGCACTTGTGCTGCGACATGCTGCTGTTTGAACCCCTCCAGCTACG 1920
Qy 1921 CACCGTGTGTGAAGCTACAGACTCAATGTGCTTTTGTGATGTGGCGCCCTCCCTGC 1980
Db 1921 CACCGTGTGTGAAGCTACAGACTCAATGTGCTTTTGTGATGTGGCGCCCTCCCTGC 1980
Qy 1981 CCGCGAATTTTCTCTGCAATGAGACGTGCGGTTCTAGCTGTGAAGCCCAATGACAGTT 2040
Db 1981 CCGCGAATTTTCTCTGCAATGAGACGTGCGGTTCTAGCTGTGAAGCCCAATGACAGTT 2040
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Db 1981 CCGCGAATTTTCTCTGCAATGAGACGTGCGGTTCTTACCTGTGAGACCCCAAGTACAGTT 2040
Qy 2041 AGTGTGGTGCTGCTGCGCTGCGCGCGGAGATGCGATGACTGTGACCTGAGAGTCTTGT 2100
Db 2041 AGTGTGGTGCTGCTGCGCTGCGCGCGGAGATGCGATGACTGTGACCTGAGAGTCTTGT 2100
Qy 2101 GTAACACAGACGACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2140
Db 2101 GTAACACAGACGACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2140

RESULT 3
AAT64542
ID AAT64542 standard; cDNA; 2137 BP.
XX
AC AAT64542;
XX
DT 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
XX
DE NADP-specific glutamate dehydrogenase alpha-subunit precursor cDNA.
XX
KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW chloroplast; transgenic plant; ds.
XX
OS Chlorella sorokiniana; strain UTEX 1230.
XX
FH Key Location/Qualifiers
FT CDS 30..1610
FT /*tag= a
FT translat_peptide 30..149
FT /*tag= b
FT mat_peptide 150..1607
FT /*tag= c

XX
PN W09712983-A1.
XX
PD 10-APR-1997.
XX
PE 03-OCT-1996; 96WO-US015921.
XX
PR 06-OCT-1995; 95US-00541033.
XX
PA (UYFL ) UNIV FLORIDA.
XX
PI Schmidt RR, Miller P;
XX
DR WPI; 1997-226226/20.
XX
DR P-PSDB; AAM15407.
XX
PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT plant cells.
XX
PS Claim 2; Page 40-41; 61p; English.
XX
CC cDNA clones (AAT64542 and AAT64543) respectively code for the alpha
CC subunit (AAM15407) and beta subunit (AAM15408) precursor proteins of an
CC ammonium-inducible, chloroplast-localised NADP-specific glutamate
CC dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were obt. by
CC ligation of 3' clone pBGD53 (AAT64531) and 5' clones pBG63 (AAT64540)
CC and pBG64 (AAT64541). The proteins are processed to yield mature alpha
CC and beta subunits (see also AAT64547-48) that comprise the active NADP-
CC GDH hexameric isoenzymes. The nitrogen metabolism of plants can be
CC modulated (pref. by increasing assimilation of inorganic N into organic
CC N) by transforming them with nucleotide sequences encoding the alpha
CC and/or beta subunits. Such plants show improved properties, e.g.
CC increased crop yield and improved stress tolerance. Heterohexamers having
CC alpha and beta subunits can be expressed that have higher
CC aminating/deaminating activity ratios (i.e. higher capacity for glutamate
CC synthesis) than homohexamers. (Updated on 17-OCT-2003 to standardise OS
CC field)
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Qy 2104 AACACGACGACTCAAAAAAAAAAAAAAAAAAAAA 2140  
Db 2101 AACACGACGACTCAAAAAAAAAAAAAAAAAAAAA 2137

RESULT 4  
ABK51020  
ID ABK51020 standard; cDNA: 2137 BP.

XX AC ABK51020;

XX DT 24-SEP-2002 (first entry)

XX NADP-glutamate dehydrogenase ligation construct pBGdc53 plus pGdc63.

KW NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;  
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;  
KW ammonia toxicity tolerance; osmotic stress tolerance; pGdc63; pGdc63;  
KW gene; ss.

XX Chlorella sorokiniana.

XX OS US2002062495-A1.

XX PD 23-MAY-2002.

XX PF 01-MAY-1998; 98US-00070844.

XX PR 01-MAY-1998; 98US-00070844.

XX PA (SCHM/) SCHMIDT R. R.

XX PI (MILL/) MILLER P.

XX PI Schmidt RR, Miller P;

XX WPI; 2002-499691/53.

XX PT Transforming a plant with a polynucleotide encoding a polypeptide with  
XX glutamate dehydrogenase activity provides a plant with modulated nitrogen  
XX metabolism useful to increase yield and ammonium and osmotic stress  
XX tolerance.

XX Example 2; Page 23; 35pp; English.

XX The invention relates to a method of modulating nitrogen metabolism in  
XX plant cells, comprising transforming a plant cell with a polynucleotide  
XX encoding a polypeptide having glutamate dehydrogenase activity, and  
XX culturing the cell to produce descendant cells which express the  
XX polypeptide. The method is used to provide plants with increased yield,  
XX improved ammonium assimilation properties, increased tolerance to ammonia  
XX toxicity, improved osmotic stress tolerance and improved composition. The  
XX present sequence represents the coding sequence of Chlorella sorokiniana  
XX NADP-glutamate dehydrogenase ligation construct of pBGdc53 plus pGdc63,  
XX used in the method of the invention

XX Sequence 2137 BP; 416 A; 732 C; 632 G; 357 T; 0 U; 0 Other;

Qy Query Match 99.9%; Score 2137; DB 6; Length 2137;  
Db Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTTTCTGCTCGCCCTCTCTCGCTCCGCGCATGACAGCCGCTCTGTCGCAAGCCTATCG 63  
Db 1 CTTTCTGCTCGCCCTCTCTCGCTCCGCGCATGACAGCCGCTCTGTCGCAAGCCTATCG 60  
Qy 64 TGGCGCGCCCGCTGCGCGCAAGCCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 123  
Db 61 TGGCGCGCCCGCTGCGCGCAAGCCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 120  
Qy 124 GCTCGCGCAAGCGGATGCGCGCGCAAGCGCGCTGCGCGCGGATGCGCGCGCA 183  
Db 121 GCTCGCGCAAGCGGATGCGCGCGCAAGCGCGCTGCGCGCGGATGCGCGCGCA 180

Qy 184 TGAACGCCAACCCACCGCGGACTTACCGCGCTGAGAAAGCGGTGAAGACAGATGCGCA 243  
Db 181 TGAACGCCAACCCACCGCGGACTTACCGCGCTGAGAAAGCGGTGAAGACAGATGCGCA 240  
Qy 244 AGCGGGGCACTGAGGGCTGTGTGACAGCGCATCAAGAAACCCCGACGTGCCCACTGCTGA 303  
Db 241 AGCGGGGCACTGAGGGCTGTGTGACAGCGCATCAAGAAACCCCGACGTGCCCACTGCTGA 300  
Qy 304 CCGAGATCTTCATGAAGAACCCCGAGCAGAGAGATTATGACAGCGGGTGCAGAGGTG 363  
Db 301 CCGAGATCTTCATGAAGAACCCCGAGCAGAGAGATTATGACAGCGGGTGCAGAGGTG 360  
Qy 364 CCGTCTCCCTGACAGCCCGCTGTGAGAAAGCGCCCGAGCTGTGCCCATTTCAAGAGA 423  
Db 361 CCGTCTCCCTGACAGCCCGCTGTGAGAAAGCGCCCGAGCTGTGCCCATTTCAAGAGA 420  
Qy 424 TCGTTGAGCTGAGCGGCTGATACCTTCCGCGTGTCTGTGCTGTGAGAGAGCGCGCA 483  
Db 421 TCGTTGAGCTGAGCGGCTGATACCTTCCGCGTGTCTGTGCTGTGAGAGAGCGCGCA 480  
Qy 484 TGAAGTCAACCGCGGCTTCCGCGTGAAGTCTGTCGCGCATGCGCCCTTCAAGAGGCG 543  
Db 481 TGAAGTCAACCGCGGCTTCCGCGTGAAGTCTGTCGCGCATGCGCCCTTCAAGAGGCG 540  
Qy 544 GCGTGCCTTCAACCCCTCCGTGAACCTGTCCATCATGAAGTTCTTTGCTTTGAGAGA 603  
Db 541 GCGTGCCTTCAACCCCTCCGTGAACCTGTCCATCATGAAGTTCTTTGCTTTGAGAGA 600  
Qy 604 TCTTCAAGAACAGCTGACCAACCTCGGCAATGAGCGCGCGCAAGCGGCTCCGACTTCG 663  
Db 601 TCTTCAAGAACAGCTGACCAACCTCGGCAATGAGCGCGCGCAAGCGGCTCCGACTTCG 660  
Qy 664 ACCCAAGGCGAAGAGAGAGAGCGGAGGTGATGCGCTTCTGCAATCTTTCATGACCGAG 723  
Db 661 ACCCAAGGCGAAGAGAGAGAGGTGATGCGCTTCTGCAATCTTTCATGACCGAGC 720  
Qy 724 TGCAGCGCACATCACTACGTGACAGAGCGTGCCTCCGCGGCAATGAGCGGTGCGCG 783  
Db 721 TGCAGCGCACATCACTACGTGACAGAGCGTGCCTCCGCGGCAATGAGCGGTGCGCG 780  
Qy 784 GCGAGATTGGCTACCTTTTGGCCAGTACAAAGGCGCATCAAGAACTTACACCGGCGTGC 843  
Db 781 GCGAGATTGGCTACCTTTTGGCCAGTACAAAGGCGCATCAAGAACTTACACCGGCGTGC 840  
Qy 844 TGAACCCGAAGGCGCAAGATGATGCGCGCTCCGAGATCCGCCGAGCGCAACGCGTACG 903  
Db 841 TGAACCCGAAGGCGCAAGATGATGCGCGCTCCGAGATCCGCCGAGCGCAACGCGTACG 900  
Qy 904 GCGCGGTGCTGTTTGTGAGAACGTGCTGAAGAACAGGCGAGAGCTTCAAGGCGAAGC 963  
Db 901 GCGCGGTGCTGTTTGTGAGAACGTGCTGAAGAACAGGCGAGAGCTTCAAGGCGAAGC 960  
Qy 964 GCTGCCGTGTGTCTGCGCGCGGCAACGTGGCCCAAGTATGCGCGGAGACTCTGTGAGA 1023  
Db 961 GCTGCCGTGTGTCTGCGCGCGGCAACGTGGCCCAAGTATGCGCGGAGACTCTGTGAGA 1020  
Qy 1024 AGGCGCCCATGTCGTGCTGCTGCTGCTGCACTCCAGAGGCTACGTATGAGACCCCAAGGCT 1083  
Db 1021 AGGCGCCCATGTCGTGCTGCTGCTGCTGCACTCCAGAGGCTACGTATGAGACCCCAAGGCT 1080  
Qy 1084 TCAAGCGCAGACAGCTGACAGCGGTGAGAGCATGAAGAAAGAACACAGCGCCCGCA 1143  
Db 1081 TCAAGCGCAGACAGCTGACAGCGGTGAGAGCATGAAGAAAGAACACAGCGCCCGCA 1140  
Qy 1144 TCTCCAGATCAAGAGGAGAACCGCGGTGATATGTGGCGGACCCCGCAACCTTGGAGAGC 1203  
Db 1141 TCTCCAGATCAAGAGGAGAACCGCGGTGATATGTGGCGGACCCCGCAACCTTGGAGAGC 1200  
Qy 1204 TGAAGTGCAGAGTGAAGATGAGCTTCCCTGCGCGCAACCCAGAAAGAGATGATGAGAGC 1263  
Db 1201 TGAAGTGCAGAGTGAAGATGAGCTTCCCTGCGCGCAACCCAGAAAGAGATGATGAGAGC 1260  
Qy 1264 ACGCCGAGCTGTGATCAAGACAGGCTGACAGTACGTGTGAAGGCGCCCAATGCGCTT 1323

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Db      1261  ACGCCGAGCTGCTGATCAAGCAGCGCTGCAGTAGTGAGAGGCGCCAAAGTGCCT 1320
Qy      1324  CCACCAACGAGGCGCATCCACAAATACAAAGGCGGATCATCTACTGCCCCGCAAG 1383
Db      1321  CCACCAACGAGGCGCATCCACAAATACAAAGGCGGATCATCTACTGCCCCGCAAG 1380
Qy      1384  CGGCGCAACGCGGCGGCGGTGCGGCTCAGCGGCTTGAGATGACCGAAGCCGATGAGCC 1443
Db      1381  CGGCGCAACGCGGCGGCGGTGCGGCTCAGCGGCTTGAGATGACCGAAGCCGATGAGCC 1440
Qy      1444  TGAACCTGAGCTCGGAGAGAGTTCCGCAAAAGCTGAGCGCATATGAAGACATCTACG 1503
Db      1441  TGAACCTGAGCTCGGAGAGAGTTCCGCAAAAGCTGAGCGCATATGAAGACATCTACG 1500
Qy      1504  ACTCCGCGATGAGGCGGCTCCGCAAGATGATGTTGACTGCTGCGGCGCAACATCG 1563
Db      1501  ACTCCGCGATGAGGCGGCTCCGCAAGATGATGTTGACTGCTGCGGCGCAACATCG 1560
Qy      1564  CGGCGCTTACCAAGGTGCTGATGCGCTCAAGGCGCCAGGCGCTTTAAAGCTGCCAG 1623
Db      1561  CGGCGCTTACCAAGGTGCTGATGCGCTCAAGGCGCCAGGCGCTTTAAAGCTGCCAG 1620
Qy      1624  CCCAAGCCAGCGCTCACCGGCAATCCAAACCAACTCAACGCGCAAGACTTTTCGG 1683
Db      1621  CCCAAGCCAGCGCTCACCGGCAATCCAAACCAACTCAACGCGCAAGACTTTTCGG 1680
Qy      1684  AAGCGGCGCTTTTCCAGCCAGGAGCCCTCACTGCTCCCTTTCATACCTGCTATTGCC 1743
Db      1681  AAGCGGCGCTTTTCCAGCCAGGAGCCCTCACTGCTCCCTTTCATACCTGCTATTGCC 1740
Qy      1744  GCGCGCGCCCTGCAATTCACCCCAAGAAAGTAAAGGCGCACTGACATGACGACGG 1803
Db      1741  GCGCGCGCCCTGCAATTCACCCCAAGAAAGTAAAGGCGCACTGACATGACGACGAG 1800
Qy      1804  CTATTTTTCGCGACGCGGCTCAACCCGAGAGCTCTCTCCCGGAGCCCTTAAGCGCT 1863
Db      1801  CTATTTTTCGCGACGCGGCTCAACCCGAGAGCTCTCTCCCGGAGCCCTTAAGCGCT 1860
Qy      1864  GAGCTCGCGCGGACTTTCCTGCGCATGCTCGGTTTGAACCCCTTCAGTCTAACCCAC 1923
Db      1861  GAGCTCGCGCGGACTTTCCTGCGCATGCTCGGTTTGAACCCCTTCAGTCTAACCCAC 1920
Qy      1924  CCTTTTTCGAGGCTTCAAGCTCAATGCTTTTAAAGTAAAGTGGCGCCCTTCTGCCCC 1983
Db      1921  CCTTTTTCGAGGCTTCAAGCTCAATGCTTTTAAAGTAAAGTGGCGCCCTTCTGCCCC 1980
Qy      1984  CGAATTTTTCGCGATGAGAGTGGGCTTCTAGGCTGAGCCCAAGTGAAGTAACTAGT 2043
Db      1981  CGAATTTTTCGCGATGAGAGTGGGCTTCTAGGCTGAGCCCAAGTGAAGTAACTAGT 2040
Qy      2044  GTGCGTGCCTTGCCTGCGCTGCGCCGCGGATGCGATCTGTGACCTGAGAGTCTTGCTA 2103
Db      2041  GTGCGTGCCTTGCCTGCGCTGCGCCGCGGATGCGATCTGTGACCTGAGAGTCTTGCTA 2100
Qy      2104  AACGCGAGCTCAAAAAAAAAAAAAAAAAAAAAA 2140
Db      2101  AACGCGAGCTCAAAAAAAAAAAAAAAAAAAAAA 2137

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## RESULT 5

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AAAT64530
ID      AAAT64530 standard; cDNA; 2099 BP.
AC      AAAT64530;
XX      17-OCT-2003 (revised)
DT      10-JUL-1997 (first entry)
XX      NADP-specific glutamate dehydrogenase beta-subunit precursor cDNA.
DE      Glutamate dehydrogenase; NADP-GDH; algae; nitrogen metabolism;
KM      chloroplast; transgenic plant; de.

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XX      OS      Chlorella sorokiniana; strain UTEX 1230.
XX      FH      Key
XX      FT      CDS
XX      FT      Location/Qualifiers
XX      FT      33..1571
XX      FT      /*tag= a
XX      FT      translat_peptide 33..140
XX      FT      /*tag= b
XX      FT      mat_peptide 141..1568
XX      FT      /*tag= c
XX      PN      W09712983-A1.
XX      PD      10-APR-1997.
XX      PE      03-OCT-1996; 96WO-US015921.
XX      PR      06-OCT-1995; 95US-00541033.
XX      PA      (UFL ) UNIV FLORIDA.
XX      PI      Schmidt RR, Miller P;
XX      DR      WPI; 1997-226226/20.
XX      DR      P-PSDB; AAM15408.
XX      PT      DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
XX      PT      sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
XX      PT      plant cells.
XX      PS      Claim 2; Page 29-32; 61pp; English.
XX      CC      cDNA clones (AAAT64529 and AAAT64530) respectively code for the alpha
XX      CC      subunit (AAM15407) and beta subunit (AAM15408) precursor proteins of an
XX      CC      ammonium-inducible, chloroplast-localised NADP-specific glutamate
XX      CC      dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were deposited in
XX      CC      E. coli DH5alpha as ATCC 69925 and 69926, respectively. The precursor
XX      CC      proteins are processed to mature alpha and beta subunits (see also
XX      CC      AAAT64547-48) that comprise active NADP-GDH hexameric isoenzymes. The
XX      CC      nitrogen metabolism of plants can be modulated (pref. increasing the
XX      CC      assimilation of inorganic nitrogen into organic nitrogen) by transforming
XX      CC      them with nucleotide sequences encoding the alpha and/or beta subunits.
XX      CC      Such plants show improved properties, e.g. increased crop yield and
XX      CC      improved stress tolerance. Heterohexamers having alpha and beta subunits
XX      CC      can be expressed that have higher amulating/deamulating activity ratios
XX      CC      (i.e. higher capacity for glutamate synthesis) than homohexamers.
XX      CC      (Updated on 17-OCT-2003 to standardise OS field)
XX      SQ      Sequence 2099 BP; 416 A; 713 C; 616 G; 354 T; 0 U; 0 Other;

Query Match      95.6%; Score 2046; DB 2; Length 2099;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2098; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

Qy      1      CTCCTTTCTGTCGCGCCCTCTCTCGTCCGCGCAAGACGCGCTGTGCGCAAGCTTA 60
Db      1      CTCCTTTCTGTCGCGCCCTCTCTCGTCCGCGCAAGACGCGCTGTGCGCAAGCTTA 60
Qy      61      TCGTGCGCGCGCGCTGCGGCAAGCGCGCGCTGCTGCGCGCGTGCCTGCGCGTGG 120
Db      61      TCGTGCGCGCGCGCTGCGGCAAGCGCGCGCTGCTGCGCGCGTGCCTGCGCGTGG 120
Qy      121      TCGGCTTCGCGCAAGCGGATGTCGCGCCCAAGCGCGTCTGCTGAGAGAGATCTTCG 180
Db      121      TCGGCTTCGCGCAAGCGGATGTCGCGCCCAAGCGCGTCTGCTGAGAGAGATCTTCG 180
Qy      181      CGATGACGCGCAACGCGGCACTTCAAGCGCGCTGCGAAGAGCGGTAAAGATGAGCCA 240
Db      181      CGATGACGCGCAACGCGGCACTTCAAGCGCGCTGCGAAGAGCGGTAAAGATGAGCCA 240
Qy      241      CCAAGCGGCGCACTGAGGCGCTGTCGACGCGCATCAAGAACCCCGAGCTGCGCAGCTGC 300
Db      241      CCAAGCGGCGCACTGAGGCGCTGTCGACGCGCATCAAGAACCCCGAGCTGCGCAGCTGC 300
Qy      300      CCAAGCGGCGCACTGAGGCGCTGTCGACGCGCATCAAGAACCCCGAGCTGCGCAGCTGC 358
Db      300      CCAAGCGGCGCACTGAGGCGCTGTCGACGCGCATCAAGAACCCCGAGCTGCGCAGCTGC 358

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QY 301 TGACCGAGATCTTTCATGAAAGGACCCGAGCAGCAGATTTCATGCAAGCGGTGCGCAGG 360  
Dd 259 TGAACGAGATCTTTCATGAAAGGACCCGAGCAGCAGATTTCATGCAAGCGGTGCGCAGG 318  
QY 361 TGGCCGCTCTCCCTGAGCGCCGCTGTTTCAAGAAAGCCGCCGAGCTGCTCCCTTCAAGC 420  
Dd 319 TGGCCGCTCTCCCTGAGCGCCGCTGTTTCAAGAAAGCCGCCGAGCTGCTCCCTTCAAGC 378  
QY 421 AGATGTTGAGCTGAGCGCGTGAATCACTTCGCGGCTGCTTGGCTGGAAGCAGCGCGCA 480  
Dd 379 AGATGTTGAGCTGAGCGCGTGAATCACTTCGCGGCTGCTTGGCTGGAAGCAGCGCGCA 438  
QY 481 ACCTGAGGTCAACCGCGGCTTCCGCGTGCAGTACTGCTCCGCAATCGGCGCTTCAAGG 540  
Dd 439 ACCTGAGGTCAACCGCGGCTTCCGCGTGCAGTACTGCTCCGCAATCGGCGCTTCAAGG 498  
QY 541 GCGGCGTGCCTTCCACCCCTCCGTTGAACCTGTGCAATCAATGAATTCCTTGCCTTGAAC 600  
Dd 499 GCGGCGTGCCTTCCACCCCTCCGTTGAACCTGTGCAATCAATGAATTCCTTGCCTTGAAC 558  
QY 601 AGATCTTCAAGAAAGCGCTGACCACTTGGCCATGAGGCGCGGAAAGGCGGCTCCGACT 660  
Dd 559 AGATCTTCAAGAAAGCGCTGACCACTTGGCCATGAGGCGCGGAAAGGCGGCTCCGACT 618  
QY 661 TCGACCCCAAGGCGAAGAGCAGCGCGAGGTGATGCGCTTTCGCAAGTCTTCAATGACG 720  
Dd 619 TCGACCCCAAGGCGAAGAGCAGCGCGAGGTGATGCGCTTTCGCAAGTCTTCAATGACG 678  
QY 721 AGCTGACGCGCACAATCACTGCTAGTGAAGAGCTGCGCGCGCGGCAATCGGCGTGGCG 780  
Dd 679 AGCTGACGCGCACAATCACTGCTAGTGAAGAGCTGCGCGCGCGGCAATCGGCGTGGCG 738  
QY 781 CGCGGAGATTGGCTACCTTTTCCGCGCAGTACCAAGCGCATCAAGAACTTCAACCGGCG 840  
Dd 739 CGCGGAGATTGGCTACCTTTTCCGCGCAGTACCAAGCGCATCAAGAACTTCAACCGGCG 798  
QY 841 TGCTGACCCCGAAGGCGCGAGAGTATGGCGGCTCCGAGATCGCCCGAGGCGCACCGGCT 900  
Dd 799 TGCTGACCCCGAAGGCGCGAGAGTATGGCGGCTCCGAGATCGCCCGAGGCGCACCGGCT 858  
QY 901 ACGGCGCGCTGCTGTTTGTGAGAACTGTGTAAGAGCAAGGCGGAGCTTCAAGGCA 960  
Dd 859 ACGGCGCGCTGCTGTTTGTGAGAACTGTGTAAGAGCAAGGCGGAGCTTCAAGGCA 918  
QY 961 AGCGCTGCTGTTGTTGCGCGGAGCAAGTGGCGGCTGCTGCTGCTG 1020  
Dd 919 AGCGCTGCTGTTGTTGCGCGGAGCAAGTGGCGGCTGCTGCTGCTGCTG 978  
QY 1021 AGAAGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
Dd 979 AGAAGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038  
QY 1081 GCTTCAAGCGCGGAGAGCTGAGCGGCTGAGAGCATGTAAGAGAGAGAGAGAGAGAGAGAG 1140  
Dd 1039 GCTTCAAGCGCGGAGAGCTGAGCGGCTGAGAGCATGTAAGAGAGAGAGAGAGAGAGAG 1098  
QY 1141 GCATCTCGAGTACAAGAGGACACCGCGGTATGTTGGGAGACCGCGCAAGGCTTGGG 1200  
Dd 1099 GCATCTCGAGTACAAGAGGACACCGCGGTATGTTGGGAGACCGCGCAAGGCTTGGG 1158  
QY 1201 AGCTGACTGCGAGAGTGAATGCGCTTCCCTGCGCAGCCAGAAAGAGATGATGAGC 1260  
Dd 1159 AGCTGACTGCGAGAGTGAATGCGCTTCCCTGCGCAGCCAGAAAGAGATGATGAGC 1218  
QY 1261 AGAAGCGCGAGCTGCTGATCAAGCAAGCGCTGCGAGTACTGTGTGAGAGGCGCCAAATGC 1320  
Dd 1219 AGAAGCGCGAGCTGCTGATCAAGCAAGCGCTGCGAGTACTGTGTGAGAGGCGCCAAATGC 1278  
QY 1321 CCTCAACAAGGAGGCGATCAACAAGTACAAGAGGCGGAGATCTACTGCGCGGCA 1380  
Dd 1279 CCTCAACAAGGAGGCGATCAACAAGTACAAGAGGCGGAGATCTACTGCGCGGCA 1338

QY 1381 AGCGCGCAACGCCGCGCGCTGCGCTGAGCGGCTTGAAGATGATCCAGAAACCGCATGA 1440  
Dd 1339 AGCGCGCAACGCCGCGCGCTGCGCTGAGCGGCTTGAAGATGATCCAGAAACCGCATGA 1398  
QY 1441 GCCTGAATGGAATCCGAGAGAGGTTTCGAGCAAGCTGAGCGCATGTAAGAGATCT 1500  
Dd 1399 GCGTGAATGGAATCCGAGAGAGGTTTCGAGCAAGCTGAGCGCATGTAAGAGATCT 1458  
QY 1501 ACAGCTCCGCAATGAGGCGCTGCGCGAGATTAATGTTGAACCTGCTGCGGCGCAACA 1560  
Dd 1459 ACAGCTCCGCAATGAGGCGCTGCGCGAGATTAATGTTGAACCTGCTGCGGCGCAACA 1518  
QY 1561 TCGCGGCTTCAACCAAGTGGCTGATGCGCTCAAGCGCGAGGCGCTGTTAAGCTGCC 1620  
Dd 1519 TCGCGGCTTCAACCAAGTGGCTGATGCGCTCAAGCGCGAGGCGCTGTTAAGCTGCC 1578  
QY 1621 AGGCGCAAGGCGGCTCAACCGGCAATCCAAACCAACCACTCAAGGCGGAGGCTTTT 1680  
Dd 1579 AGGCGCAAGGCGGCTCAACCGGCAATCCAAACCAACCACTCAAGGCGGAGGCTTTT 1638  
QY 1681 CGGAAGCGGCGCTTTTCCAGCAGGCGCTTCACTGCGCTTTCATTAACCTGCTATT 1740  
Dd 1639 CGGAAGCGGCGCTTTTCCAGCAGGCGCTTCACTGCGCTTTCATTAACCTGCTATT 1698  
QY 1741 GCGCGGCTGCGCTGCAATTCACCCAGAGAACTAGCGGCACTTGAATGATCAGGA 1800  
Dd 1699 GCGCGGCTGCGCTGCAATTCACCCAGAGAACTAGCGGCACTTGAATGATCAGGA 1758  
QY 1801 CGGCTATTTTTCGCGAGCGCGGCTCACCCGAGAGGCTCTCCCGGAGGCTTAAGC 1860  
Dd 1759 CGGCTATTTTTCGCGAGCGCGGCTCACCCGAGAGGCTCTCTCCCGGAGGCTTAAGC 1818  
QY 1861 GCTGACGTCGCGCGCACTTTGCTCGCACATGCTGCTGTTTGAACCCCTTCAAGTAC 1920  
Dd 1819 GCTGACGTCGCGCGCACTTTGCTCGCACATGCTGCTGTTTGAACCCCTTCAAGTAC 1878  
QY 1921 CACCTGTTGAAAGCTTACCAAGTCAATTCCTTTAGTGTATGTCGCGGCTCTG 1980  
Dd 1879 CACCTGTTGAAAGCTTACCAAGTCAATTCCTTTAGTGTATGTCGCGGCTCTG 1938  
QY 1981 CCGGAAATTTTCCGCGCATGAGAAGTGGGCTTCTAGCTGATGAGCCCAAGTAGCAGTT 2040  
Dd 1939 CCGGAAATTTTCCGCGCATGAGAAGTGGGCTTCTAGCTGATGAGCCCAAGTAGCAGTT 1998  
QY 2041 AGTGTGCTGCTTGCCTGCGCTGCGTCCGCGAGTGCATCTGTGACCTGAGAGTCTGT 2100  
Dd 1999 AGTGTGCTGCTTGCCTGCGCTGCGTCCGCGAGTGCATCTGTGACCTGAGAGTCTGT 2058  
QY 2101 GTAAACAGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140  
Dd 2059 GTAAACAGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2098

RESULT 6  
ABK51008  
ID ABK51008 standard; cDNA; 2099 BP.  
XX  
AC ABK51008;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
Dd cDNA encoding NADP-glutamate dehydrogenase beta subunit.  
XX  
DE NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;  
Dd nitrogen metabolism; plant; ammonium assimilation; transgenic;  
XX ammonia toxicity tolerance; osmotic stress tolerance; gene; ss.  
XX  
OS Chlorella sorokiniana.  
XX  
FH Key Location/Qualifiers  
FT 33..1571  
FT CDS  
FT /product= "NADP-specific glutamate dehydrogenase beta



FT subunit  
XX US2002062495-A1.  
XX 23-MAY-2002.  
XX 01-MAY-1998; 98US-00070844.  
XX 01-MAY-1998; 98US-00070844.  
XX (SCHMIDT R R.  
XX (MILLER P.  
XX Schmidt RR, Miller P;  
XX WPI, 2002-499691/53.  
XX P-PSDB; AAU98951.  
XX  
XX Transferring a plant with a polynucleotide encoding a polypeptide with  
XX glutamate dehydrogenase activity provides a plant with modulated nitrogen  
XX metabolism useful to increase yield and ammonium and osmotic stress  
XX tolerance.  
XX  
XX Disclosure; Page 15-17; 35pp; English.  
XX  
XX The invention relates to a method of modulating nitrogen metabolism in  
XX plant cells, comprising transforming a plant cell with a polynucleotide  
XX encoding a polypeptide having glutamate dehydrogenase activity, and  
XX culturing the cell to produce descendant cells which express the  
XX polypeptide. The method is used to provide plants with increased yield,  
XX improved ammonium assimilation properties, increased tolerance to ammonia  
XX toxicity, improved osmotic stress tolerance and improved composition. The  
XX present sequence represents the coding sequence of Chlorella sorokiniana  
XX NADP-glutamate dehydrogenase beta subunit, used in the method of the  
XX invention  
XX  
XX Sequence 2099 BP; 416 A; 713 C; 616 G; 354 T; 0 U; 0 Other;  
XX  
XX Query Match 95.6%; Score 2046; DB 6; Length 2099;  
XX Best Local Similarity 98.0%; Pred. No. 0;  
XX Matches 2098; Conservative 0; Mismatches 0; Indels 42; Gaps 1;  
XX  
QY 1 CTCCTTTGCTGCGCCCTCTGCTGCGCCGATGCAAGCCGCTGCGCAAGCCTA 60  
Db 1 CTCCTTTGCTGCGCCCTCTGCTGCGCCGATGCAAGCCGCTGCGCAAGCCTA 60  
QY 61 TCGTGACCGCCCGCTGCGGACCGCCGCGCTGCGCGCTGCGCGCTGCGCGT 120  
Db 61 TCGTGACCGCCCGCTGCGGACCGCCGCGCTGCGCGCTGCGCGCTGCGCGT 120  
QY 121 TCCGCTCCGCAAGCGCATGTCGCGCCAGGCGCTGCTGCGTGAAGAGCATCTCC 180  
Db 79 TCCGCTCCGCAAGCGCATGTCGCGCCAGGCGCTGCTGCGTGAAGAGCATCTCC 138  
QY 181 CGATGGAAGCAACCGCGGCACTTCAAGCGCTGCAAGAGCGGTGAAGAGCATG 240  
Db 139 CGATGGAAGCAACCGCGGCACTTCAAGCGCTGCAAGAGCGGTGAAGAGCATG 198  
QY 241 CCAAGCGCGGCACTGAGGCGCTGTCAGCGCATCAAGACCCGACGTGCGCGAGTGC 300  
Db 199 CCAAGCGCGGCACTGAGGCGCTGTCAGCGCATCAAGACCCGACGTGCGCGAGTGC 258  
QY 301 TGACCGAGATCTTCAAGAGACCGGAGACAGAGAGTTCATGAGCGGTGCGAGG 360  
Db 259 TGACCGAGATCTTCAAGAGACCGGAGACAGAGAGTTCATGAGCGGTGCGAGG 318  
QY 361 TGGCGCTCTCCGTCAGCGCCGCTGTCGAGAGAGCGCCGAGAGTGTGCGCATCTTCAAGC 420  
Db 319 TGGCGCTCTCCGTCAGCGCCGCTGTCGAGAGAGCGCCGAGAGTGTGCGCATCTTCAAGC 378  
QY 421 AGATGTTGAGCGCTGAGCGCGTATCATCTTCCGCGTGTCTGCGTGAAGAGCGCGCA 480  
Db 379 AGATGTTGAGCGCTGAGCGCGTATCATCTTCCGCGTGTCTGCGTGAAGAGCGCGCA 438

QY 481 ACCTGAGGTCAACCGGCGCTTCCGCGTGAAGTACTGCTCCGCGCATGCGGCCCTACAAG 540  
Db 439 ACCTGAGGTCAACCGGCGCTTCCGCGTGAAGTACTGCTCCGCGCATGCGGCCCTACAAG 498  
QY 541 GCGGCTGCGCTTCCACCCCTCCGTGAACCTGTCAATCATGAGTTCCTTCCCTTGAAGC 600  
Db 499 GCGGCTGCGCTTCCACCCCTCCGTGAACCTGTCAATCATGAGTTCCTTCCCTTGAAGC 558  
QY 601 AGATCTTCAAGACAGCTTGAACACCTGCGCATAGGCGCGGCAAGGCGGCTCCGACT 660  
Db 559 AGATCTTCAAGACAGCTTGAACACCTGCGCATAGGCGCGGCAAGGCGGCTCCGACT 618  
QY 661 TCGACCCCAAGGAGGAGGAGCGGAGGAGTGTGCGCTTGCAGTCTTCAATGACG 720  
Db 619 TCGACCCCAAGGAGGAGGAGGAGGAGTGTGCGCTTGCAGTCTTCAATGACG 678  
QY 721 AGCTGACGCGCACAATGACGTCAGGAGAGCTGCGCGCGGACATCGGCGTGAAGC 780  
Db 679 AGCTGACGCGCACAATGACGTCAGGAGAGCTGCGCGCGGACATCGGCGTGAAGC 738  
QY 781 CGCGGAGATTGCTACTCTTTCCGCGCATGACAGCGCATCAAGAACTTACACCGCG 840  
Db 739 CGCGGAGATTGCTACTCTTTCCGCGCATGACAGCGCATCAAGAACTTACACCGCG 798  
QY 841 TGTGACCCCGAAGGCGCAGAGTATGCGCGCTCGAGATCGCGCCGAGGCGCACCGGCT 900  
Db 799 TGTGACCCCGAAGGCGCAGAGTATGCGCGCTCGAGATCGCGCCGAGGCGCACCGGCT 858  
QY 901 ACAGCGCGCTGCTTTTGTGAGAGAGCTGCAAGAGCAAGAGGCGAGCTTCAAGGCA 960  
Db 859 ACAGCGCGCTGCTTTTGTGAGAGAGCTGCAAGAGCAAGAGGCGAGCTTCAAGGCA 918  
QY 961 AGCGCTGCTGTGTGCGCGGCGCAAGCTGCGCAAGTCTGCGCGAGCTGCTGTG 1020  
Db 919 AGCGCTGCTGTGTGCGCGGCGCAAGCTGCGCAAGTCTGCGCGAGCTGCTGTG 978  
QY 1021 AGAAGGCGCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
Db 979 AGAAGGCGCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038  
QY 1081 GCTTCAAGCGGAGAGCTGAGAGCGGTGCAAGATGAAGAAAGAAAGAAAGAGCGGCC 1140  
Db 1039 GCTTCAAGCGGAGAGCTGAGAGCGGTGCAAGATGAAGAAAGAAAGAAAGAGCGGCC 1098  
QY 1141 GCATCTCGAGTACAGAGCGACACCGCGGTGATGATGAGGCGAGCGCGCAAGCTTGG 1200  
Db 1099 GCATCTCGAGTACAGAGCGACACCGCGGTGATGATGAGGCGAGCGCGCAAGCTTGG 1158  
QY 1201 AGCTGAGTCCGAGTGAATGCGCTTCCCTGCGGCAACCAAGAGAGATGATGAGC 1260  
Db 1159 AGCTGAGTCCGAGTGAATGCGCTTCCCTGCGGCAACCAAGAGAGATGATGAGC 1218  
QY 1261 ACAGCGCGAGCTGTATCAAGAGCGGCTGCAAGTACGTGTGAAGGCGCCCAAGTGC 1320  
Db 1219 ACAGCGCGAGCTGTATCAAGAGCGGCTGCAAGTACGTGTGAAGGCGCCCAAGTGC 1278  
QY 1321 CCTCACAAGAGAGGCAATCCAAAGTACAAAGAGCGGATCATCTTATGCTCCCGCA 1380  
Db 1279 CCTCACAAGAGAGGCAATCCAAAGTACAAAGAGCGGATCATCTTATGCTCCCGCA 1338  
QY 1381 AGGCGGCGCAAGCGGCGGCGGTGCGGTCAAGCGGCTGAGATGAAGCCGAGTGA 1440  
Db 1339 AGGCGGCGCAAGCGGCGGCGGTGCGGTCAAGCGGCTGAGATGAAGCCGAGTGA 1398  
QY 1441 GCTGAAGTGAAGTGGAGAGGTTGCGGCAAGCTGAGCGGATCATGAAGAGCATCT 1500  
Db 1399 GCTGAAGTGAAGTGGAGAGGTTGCGGCAAGCTGAGCGGATCATGAAGAGCATCT 1458  
QY 1501 ACAGCTCGCGCATGAGGCGGTCCGCAAGTACAAAGTGTGACCTGCGGCGCCCAAG 1560  
Db 1459 ACAGCTCGCGCATGAGGCGGTCCGCAAGTACAAAGTGTGACCTGCGGCGCCCAAG 1518

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Qy 1561 TCGCGGGCTTCACCAAGGTGCTGATGCTCAAGAGCCGAGGGCGCTGTTTAAGCTGCCC 1620
    |||
Db 1519 TCGGGGGCTTACCAAGGTGCTGATGCTCAAGAGCCGAGGGCGCTGTTTAAGCTGCCC 1578
Qy 1621 AGCGCCCAAGCGGCTCACCAGCAATCAACCACTCAAGCGCCAGACCTTTT 1680
    |||
Db 1579 AGCGCCCAAGCGGCTCACCAGCAATCAACCACTCAAGCGCCAGACCTTTT 1638
Qy 1681 CGGAAGGGGGCGCTTTTCCAGAGGGGCGCTCAACCGGCTTCAATTAACCGCTATT 1740
    |||
Db 1639 CGGAAGGGGGCGCTTTTCCAGAGGGGCGCTCAACCGGCTTCAATTAACCGCTATT 1698
Qy 1741 GCGCGCGTCCCTGTCATTCACCCCAAGAAAGTACGCGCACTTGATGTCATCAGGA 1800
    |||
Db 1699 GCGCGCGTCCCTGTCATTCACCCCAAGAAAGTACGCGCACTTGATGTCATCAGGA 1758
Qy 1801 CGGCTATTTTGTGGCGAGCGCGCTCAACCCGAGAGCTTCTCCCGAGCCCTTAAGC 1860
    |||
Db 1759 CGGCTATTTTGTGGCGAGCGCGCTCAACCCGAGAGCTTCTCCCGAGCCCTTAAGC 1818
Qy 1861 GCTGACGTCCGCGCGGACTTTGCTCGGCAATCGGCTGGTTTGAACCCCTCAGTCAAC 1920
    |||
Db 1819 GCTGACGTCCGCGCGGACTTTGCTCGGCAATCGGCTGGTTTGAACCCCTCAGTCAAC 1878
Qy 1921 CACCTGTGTGAAGCCTTACAGCTCAATTCCTTTAGTGTATGTGCGCCCTCCTGC 1980
    |||
Db 1879 CACCTGTGTGAAGCCTTACAGCTCAATTCCTTTAGTGTATGTGCGCCCTCCTGC 1938
Qy 1981 CCGCGAATTTTCTGCGCATGAGAGTGGGTTCTAGCCTGTGACCCCAAGTACAGTT 2040
    |||
Db 1939 CCGCGAATTTTCTGCGCATGAGAGTGGGTTCTAGCCTGTGACCCCAAGTACAGTT 1998
Qy 2041 AGTGGGTGCTGCTTGGCCCTGCGGCTGCGCGGAGTGGATGCTGACCTGAGAGCTTGT 2100
    |||
Db 1999 AGTGGGTGCTGCTTGGCCCTGCGGCTGCGCGGAGTGGATGCTGAGAGTGTGTGT 2058
Qy 2101 GTAAACACGACGAGTCACAAAAA 2140
    |||
Db 2059 GTAAACACGACGAGTCACAAAAA 2098
    |||

RESULT 7
AAT64543
ID AAT64543 standard; cDNA; 2096 BP.
XX AC AAT64543;
XX 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
DE NADP-specific glutamate dehydrogenase beta-subunit precursor cDNA.
XX
KM Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KM chloroplast; transgenic plant; ds.
XX
OS Chlorella sorokiniana; strain UTEX 1230.
XX
FH Key location/Qualifiers
FT CDS 30..1568
FT translat_peptide 30..146 /*tag= a
FT /*tag= b
FT mat_peptide 147..1565 /*tag= c
FT
XX
XX MO9712983-A1.
XX
XX 10-APR-1997.
XX
XX 03-OCT-1996; 96WO-US015921.
XX
XX 06-OCT-1995; 95US-00541033.
XX
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PA (UYFL ) UNIV FLORIDA.
XX
XX Schmidt RR, Miller P;
XX
XX WPI; 1997-226226/20.
DR P-PSDB; .AAW15408.
XX
XX DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
XX plant cells.
XX
XX Claim 2; Page 41-43; 61pp; English.
PS
XX
XX cDNA clones (AAT64542 and AAT64543) respectively code for the alpha
CC subunit (AAW15407) and beta subunit (AAW15408) precursor proteins of an
CC ammonium-inducible, chloroplast-localised NADP-specific glutamate
CC dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were obtd. by
CC ligation of 3' clone PBGDS3 (AAT64531) and 5' clones pGDS3 (AAT64540)
CC and pBDS64 (AAT64541). The proteins are processed to yield mature alpha
CC and beta subunits (see also AAT64547-48) that comprise the active NADP-
CC GDH hexameric isoenzymes. The nitrogen metabolism of plants can be
CC modulated (pref. by increasing assimilation of inorganic N into organic
CC N) by transforming them with nucleotide sequences encoding the alpha
CC and/or beta subunits. Such plants show improved properties, e.g.
CC increased crop yield and improved stress tolerance. Heterohexamers having
CC alpha and beta subunits can be expressed that have higher
CC ammonia/deammoniating activity ratios (i.e. higher capacity for glutamate
CC synthesis) than homohexamers. (updated on 17-OCT-2003 to standardise OS
CC field)
XX
XX
SQ Sequence 2096 BP; 416 A; 711 C; 616 G; 353 T; 0 U; 0 Other;

Query Match 95.5%; Score 2043; DB 2; Length 2096;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

Qy 4 CTTTCTGCTGCGCCTCTCTCCGTCGCCATGAGACCGGCTGTGTCGCAAGCTATCG 63
    |||
Db 1 CTTTCTGCTGCGCCTCTCTCCGTCGCCATGAGACCGGCTGTGTCGCAAGCTATCG 60
    |||
Qy 64 TGGCGCGCGCGCTGCGGCAAGCGCGCGCTGCTCGCGCGCTGCGCGCTGCGCGTGC 123
    |||
Db 61 TGGCC-----TGGCGCTGCTGC 78
    |||
Qy 124 GCTCGCGCAAGCGGAGTTCGCGCGCAAGGCGGCTGCTGAGAGACAGATCTCCGCGA 183
    |||
Db 79 GCTCGCGCAAGCGGAGTTCGCGCGCAAGGCGGCTGCTGAGAGACAGATCTCCGCGA 138
    |||
Qy 184 TGAACGCCACCAACCGGAGCTTCAAGCGGCTGCAAGAGCGGTGAGACAGATGCGACCA 243
    |||
Db 139 TGAACGCCACCAACCGGAGCTTCAAGCGGCTGCAAGAGCGGTGAGACAGATGCGACCA 198
    |||
Qy 244 AGCGGGGACACTGAGAGGCTGTGTCAGCGGATCAAGAACCCCGAGTGTCCCACTGTGA 303
    |||
Db 199 AGCGGGGACACTGAGAGGCTGTGTCAGCGGATCAAGAACCCCGAGTGTCCCACTGTGA 258
    |||
Qy 304 CCGAGATCTTCATGAGAGACCCGAGAGCAGAGAGTTCATGAGAGCGGTGCGCGAGGTGG 363
    |||
Db 259 CCGAGATCTTCATGAGAGACCCGAGAGCAGAGAGTTCATGAGAGCGGTGCGCGAGGTGG 318
    |||
Qy 364 CCGTCTCCCTGACAGCCGCTGTTCGAGAAGCGCCCGAGAGTGTCCCATTTCAAGAGA 423
    |||
Db 319 CCGTCTCCCTGACAGCCGCTGTTCGAGAAGCGCCCGAGAGTGTCCCATTTCAAGAGA 378
    |||
Qy 424 TCGTTAGCCTGAGCGCGTGTATCACTTCCGCGTGTCTTGCTGAGAGAGCGGCAACC 483
    |||
Db 379 TCGTTAGCCTGAGCGCGTGTATCACTTCCGCGTGTCTTGCTGAGAGAGCGGCAACC 438
    |||
Qy 484 TGCAGGTCAACCGCGGCTTCGCGGTGAGTACGTGTCGCGCATGCGGCGCTCAAGGGCG 543
    |||
Db 439 TGCAGGTCAACCGCGGCTTCGCGGTGAGTACGTGTCGCGCATGCGGCGCTCAAGGGCG 498
    |||
Qy 544 GCTGCGCTTCAACCCCTCCGTGAACTGTTCATCATGAAGTTCTTGCTTGAAGAGA 603
    |||
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Db 499 GCTGCGCTTCCACCCCTCCGTAACCTGTCATCATGTAAGTTCCTTTCGAGCAGA 558
Qy 604 TCTTCAAGAAAGCTGTACCAACCTTGGCCCATGGGGGGGCAAGGGGGGCTCCCATTCG 663
Db 559 TCTTCAAGAAAGCTGTACCAACCTTGGCCCATGGGGGGGCAAGGGGGGCTCCCATTCG 618
Qy 664 ACCCAAGAGGAGAGAGCAGCGGAGGTGATGCGCTTCTGCAAGTCTTTCATGACCGAGC 723
Db 619 ACCCAAGAGGAGAGAGCAGCGGAGGTGATGCGCTTCTGCAAGTCTTTCATGACCGAGC 678
Qy 724 TGACGCGGCACATCAGCTAGCTGAGAGAGTCCCGCGGAGCAATCGGCGTGGCGGC 783
Db 679 TGACGCGGCACATCAGCTAGCTGAGAGAGTCCCGCGGAGCAATCGGCGTGGCGGC 738
Qy 784 GCGAGATTGGCTACTCTTTTCGCGCCAGTACCAAGCGCATCAACAAACTACACCGGCTGC 843
Db 739 GCGAGATTGGCTACTCTTTTCGCGCCAGTACCAAGCGCATCAACAAACTACACCGGCTGC 798
Qy 844 TGACCCCGAAGGGGCGAGAGTATGGCGGCTCCGAGATCCGCGCGGCAACCGGCTACG 903
Db 799 TGACCCCGAAGGGGCGAGAGTATGGCGGCTCCGAGATCCGCGCGGCAACCGGCTACG 858
Qy 904 GCGCGCTGCTGTTTGTGAGAGACGTGCTGAAAGACAAAGGCGAGAGCTTCAAGGCGAAGC 963
Db 859 GCGCGCTGCTGTTTGTGAGAGACGTGCTGAAAGACAAAGGCGAGAGCTTCAAGGCGAAGC 918
Qy 964 GCTGCTGTGTCTGTGGCGCGGCGCAAGTGGCCAGTACTGCGCGGAGCTGCTGTGAGA 1023
Db 919 GCTGCTGTGTCTGTGGCGCGGCGCAAGTGGCCAGTACTGCGCGGAGCTGCTGTGAGA 978
Qy 1024 AGGGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
Db 979 AGGGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
Qy 1084 TCACGCGGAGACAGCTGAGCGGCTGTCAGAGCATGAAAGAAAGAAACAACAGCGCCGCA 1143
Db 1039 TCACGCGGAGACAGCTGAGCGGCTGTCAGAGCATGAAAGAAAGAAACAACAGCGCCGCA 1098
Qy 1144 TCTCCGAGTACAGAGCAGACACCGCGTGTATGTGTGGCGACCGCGCAAGCTTGTGGAGC 1203
Db 1099 TCTCCGAGTACAGAGCAGACACCGCGTGTATGTGTGGCGACCGCGCAAGCTTGTGGAGC 1158
Qy 1204 TGGAAGTGCAGGTGAGACATGCGCTTCCCTGCGGCAACCAAGAGTGCATGAGCAGC 1263
Db 1159 TGGAAGTGCAGGTGAGACATGCGCTTCCCTGCGGCAACCAAGAGTGCATGAGCAGC 1218
Qy 1264 ACGCGAGCTGTATCAAGCAGCGCTGCAAGTACGTGTGAGAGGCGCCCAACATGCCCT 1323
Db 1219 ACGCGAGCTGTATCAAGCAGCGCTGCAAGTACGTGTGAGAGGCGCCCAACATGCCCT 1278
Qy 1324 CCACCAAGAGGCGCATCCACAAGTACAAACAGCGCGCATCTTACCTCCCGGCAAGC 1383
Db 1279 CCACCAAGAGGCGCATCCACAAGTACAAACAGCGCGCATCTTACCTCCCGGCAAGC 1338
Qy 1384 CCGGCAAGCGCGGCGCTGCGGCTGCAAGCTGAGAGTACCAAGAAACCGCATGAGCC 1443
Db 1339 CCGGCAAGCGCGGCGCTGCGGCTGCAAGCTGAGAGTACCAAGAAACCGCATGAGCC 1398
Qy 1444 TGAAGTGGACTCGGAGAGGTTGCGCAAGCTGAGAGCGCATCATGAAAGACATCTTACG 1503
Db 1399 TGAAGTGGACTCGGAGAGGTTGCGCAAGCTGAGAGCGCATCATGAAAGACATCTTACG 1458
Qy 1504 ACTCCGCGCATGGGCGCTCCGCAAGTACAACTGTGACTGCGGCGCGCAACATCG 1563
Db 1459 ACTCCGCGCATGGGCGCTCCGCAAGTACAACTGTGACTGCGGCGCGCAACATCG 1518
Qy 1564 CCGGCTTCAACCAAGTGTGTATGCTGCTCAAGGCGCCAGAGGCGCTTTTAACTGCCAGG 1623
Db 1519 CCGGCTTCAACCAAGTGTGTATGCTGCTCAAGGCGCCAGAGGCGCTTTTAACTGCCAGG 1578
Qy 1624 CCAAGCGCAGGCTCAACGCGCAATCCAAACCAACCACTCAACGCGCAGAGCTTTTGGG 1683
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Db 1579 CCAAGCGCAGGCTACCGCGCAATCCAAACCAACCACTCAACGCGCAGAGCTTTTCGG 1638
Qy 1684 AAGCGGCGCTTTTCCAGCCAGGCGCTCACCGGCGCTTCAATACCTGATATGCG 1743
Db 1639 AAGCGGCGCTTTTCCAGCCAGGCGCTCACCGGCGCTTCAATACCTGATATGCG 1698
Qy 1744 GCCGTGCCCTTCAATTCACACCCCAAGAACTAGCGGCGCACTTGTATGATAGAGCAG 1803
Db 1699 GCCGTGCCCTTCAATTCACACCCCAAGAACTAGCGGCGCACTTGTATGATAGAGCAG 1758
Qy 1804 CTATTTTTCGCGACGCGGCTCAACCCGAGAGCTCTCTCCCGGAGCCCTTAAAGCGCT 1863
Db 1759 CTATTTTTCGCGACGCGGCTCAACCCGAGAGCTCTCTCCCGGAGCCCTTAAAGCGCT 1818
Qy 1864 GACGTCCGCGGCACTTTCGCGGCAATCGCTCGGTTTGAACCCCTCCAGTCAACCCAC 1923
Db 1819 GACGTCCGCGGCACTTTCGCGGCAATCGCTCGGTTTGAACCCCTCCAGTCAACCCAC 1878
Qy 1924 CCTGTTGAGAGCTTACAGGCTCAATTGCTTTAGTATGTGCGCCCTCCGCGCC 1983
Db 1879 CCTGTTGAGAGCTTACAGGCTCAATTGCTTTAGTATGTGCGCCCTCCGCGCC 1938
Qy 1984 CGAATTTTCTGCGATGAGAGCTGCGGTTCTTACCTGTGACCCCAAGTACAGTATAGT 2043
Db 1939 CGAATTTTCTGCGATGAGAGCTGCGGTTCTTACCTGTGACCCCAAGTACAGTATAGT 1998
Qy 2044 GTGCGTGCCTTTCGCTGCGGCGCGGATGCGGATACCTGTGACCTGAGAGTCTTGTGTA 2103
Db 1999 GTGCGTGCCTTTCGCTGCGGCGCGGATGCGGATGAGTACCTGTGAGAGTCTTGTGTA 2058
Qy 2104 AACAGAGAGTCAAAAAA 2140
Db 2059 AACAGAGAGTCAAAAAA 2095

RESULT 8
ABK51021
ID ABK51021 standard; cDNA; 2096 BP.
XX
AC ABK51021;
XX
DT 24-SEP-2002 (first entry)
XX
DE NADP-glutamate dehydrogenase ligation construct pBGdc53 plus pBGdc64.
XX
KW NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
KW ammonia toxicity tolerance; osmotic stress tolerance; pBGdc64; pBGdc63;
KW gene; ss.
XX
OS Chlorella sorokiniana.
XX
FN US2002062495-A1.
XX
PD 23-MAY-2002.
XX
PE 01-MAY-1998; 98US-00070844.
XX
PR 01-MAY-1998; 98US-00070844.
XX
PA (SCHMIDT R. R.
XX (MILLER P.
XX Schmidt RR, Miller P;
XX
PI WPI; 2002-499691/53.
XX
DR
XX
PT Transforming a plant with a polynucleotide encoding a polypeptide with
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
PT metabolism useful to increase yield and ammonium and osmotic stress
PT tolerance.
XX
PS Example 2; Page 24-25; 35pp; English.
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XX The invention relates to a method of modulating nitrogen metabolism in  
CC plant cells, comprising transforming a plant cell with a polynucleotide  
CC encoding a polypeptide having glutamate dehydrogenase activity, and  
CC culturing the cell to produce descendant cells which express the  
CC polypeptide. The method is used to provide plants which increase yield,  
CC improved ammonium assimilation properties, increased tolerance to ammonia  
CC toxicity, improved osmotic stress tolerance, and improved composition. The  
CC present sequence represents the coding sequence of Chlorella sorokiniana  
CC NADP-glutamate dehydrogenase ligation construct of pBDE53 plus pBDC64,  
CC used in the method of the invention

XX Sequence 2096 BP; 416 A; 711 C; 616 G; 353 T; 0 U; 0 Other;

Query Match 95.5%; Score 2043; DB 6; Length 2096;

Best Local Similarity 98.0%; Pred. No. 0; Mismatches 0; Indels 42; Gaps 1;

Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY 4 CTTTCTGCTCGCCCTCTCTCCGTCGCCATGACAGCCGCCCTGTCGCCAAGCCTATCG 63  
DB 1 CTTTCTGCTCGCCCTCTCTCCGTCGCCATGACAGCCGCCCTGTCGCCAAGCCTATCG 60  
QY 64 TGGCCGCCCCGCTGCGGCAAGCCCGCGCTGCTGCGCCGCTGCGCCGCTGCGGTC 123  
DB 61 TGGCC-----TGCGCGTGGGTC 78  
QY 124 GCTCCGCGCAAGCGGATGTCGCGCGCAAGCGCGTCTGCTGAGAGAGAGATCTCCGGA 183  
DB 79 GCTCCGCGCAAGCGGATGTCGCGCGCAAGCGCGTCTGCTGAGAGAGAGATCTCCGGA 138  
QY 184 TGAAGCGCACCAAGCGGCGATCTTCAAGCGGCTGCGAAGAGCGGTAAGATGCGCA 243  
DB 139 TGAAGCGCACCAAGCGGCGATCTTCAAGCGGCTGCGAAGAGCGGTAAGATGCGCA 198  
QY 244 AGGCGGCGACTGAGAGCGCTGCTGCAAGCGGCGATCAAGAACCGCGAGTGGCCAGCTGCA 303  
DB 199 AGGCGGCGACTGAGAGCGCTGCTGCAAGCGGCGATCAAGAACCGCGAGTGGCCAGCTGCA 258  
QY 304 CCGAGATCTTATGAGAGACCGGAGCGAGAGATTCATGACAGCGGCTGCGAGGTG 363  
DB 259 CCGAGATCTTATGAGAGACCGGAGCGAGAGATTCATGACAGCGGCTGCGAGGTG 318  
QY 364 CCGTCTCCCTGCAAGCGCGTGTTCGAGAGCGCCCGAGCTGCGCAATCTTCAAGAGA 423  
DB 319 CCGTCTCCCTGCAAGCGCGTGTTCGAGAGCGCCCGAGCTGCGCAATCTTCAAGAGA 378  
QY 424 TCGTTGAGCTGAGCGCGTGTATCACTTCGCGGTGTCTGCGTGAAGAGCGCGCAACC 483  
DB 379 TCGTTGAGCTGAGCGCGTGTATCACTTCGCGGTGTCTGCGTGAAGAGCGCGCAACC 438  
QY 484 TGAAGTCAACCGGCGGCTTCCGCGTGAATCGTCCGCCATGCGGCCCTTCAAGAGGCG 543  
DB 439 TGAAGTCAACCGGCGGCTTCCGCGTGAATCGTCCGCCATGCGGCCCTTCAAGAGGCG 498  
QY 544 GCGTCCGCTTCAACCCCTCGGTGAACCTGTCCATCATGAGATTCTTTCCTTGAAGAGA 603  
DB 499 GCGTCCGCTTCAACCCCTCGGTGAACCTGTCCATCATGAGATTCTTTCCTTGAAGAGA 558  
QY 604 TCTTCAAGAAAGCTGACACCTCTGCCATGAGGCGGCGCAAGAGGCGGCTCCGACTTTCG 663  
DB 559 TCTTCAAGAAAGCTGACACCTCTGCCATGAGGCGGCGCAAGAGGCGGCTCCGACTTTCG 618  
QY 664 ACCCAAGGGAAGAGCGAGCGAGGATGATGCGCTTTCGCAAGTCTTCAATGAACCGAGC 723  
DB 619 ACCCAAGGGAAGAGCGAGCGAGGATGATGCGCTTTCGCAAGTCTTCAATGAACCGAGC 678  
QY 724 TGAAGCGCGCAATGATGATGAGAGAGCGTCCCGCGAGCAATCGGCGTGGCGCGC 783  
DB 679 TGAAGCGCGCAATGATGATGAGAGAGCGTCCCGCGAGCAATCGGCGTGGCGCGC 738  
QY 784 GCGAGATGAGCTACTTTTGGCGGAGTGAAGCGGATCAAGAGAACTACCGGCGTGC 843  
DB 739 GCGAGATGAGCTACTTTTGGCGGAGTGAAGCGGATCAAGAGAACTACCGGCGTGC 798

QY 844 TGAACCCGAAGGCGAAGAGTATGCGGCTCCGAGATCCGCCCGAGGCCACCGGCTACG 903  
DB 799 TGAACCCGAAGGCGAAGAGTATGCGGCTCCGAGATCCGCCCGAGGCCACCGGCTACG 858  
QY 904 GCGCGGTGCTGTTTGTGAGAAAGTGTGAAGAACAGGCGGAGAGCTTCAAGGCGAAC 963  
DB 859 GCGCGGTGCTGTTTGTGAGAAAGTGTGAAGAACAGGCGGAGAGCTTCAAGGCGAAC 918  
QY 964 GCTGCTGATGTGCGGCGGCGCAAGCTGAGCCAGTACTGCGGAGAGCTGCTGTGAGA 1023  
DB 919 GCTGCTGATGTGCGGCGGCGCAAGCTGAGCCAGTACTGCGGAGAGCTGCTGTGAGA 978  
QY 1024 AGGCGCGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
DB 979 AGGCGCGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038  
QY 1084 TCAAGCGCGAGAGCTGCAAGCGGCTGCAAGAGATGAAGAAAGAACAGAGCGCGCA 1143  
DB 1039 TCAAGCGCGAGAGCTGCAAGCGGCTGCAAGAGATGAAGAAAGAACAGAGCGCGCA 1098  
QY 1144 TCTCCAGTACAAAGAGGAGACCGCGGCTGATGAGGCGAGCGCGCGCAAGCTTGGAGC 1203  
DB 1099 TCTCCAGTACAAAGAGGAGACCGCGGCTGATGAGGCGAGCGCGCGCAAGCTTGGAGC 1158  
QY 1204 TGAAGTGCAGTGAATGATGCTTCCCTGCGCGCACCAAGAGAGATGATGAGCAGC 1263  
DB 1159 TGAAGTGCAGTGAATGATGCTTCCCTGCGCGCACCAAGAGAGATGATGAGCAGC 1218  
QY 1264 ACGCGAGCTGCTGATTAAGCAAGGCTGCAAGTACGTGTGAGAGGCGCAATGCGCT 1323  
DB 1219 ACGCGAGCTGCTGATTAAGCAAGGCTGCAAGTACGTGTGAGAGGCGCAATGCGCT 1278  
QY 1324 CCAACCAAGAGGCGCATCAAGTACCAAGAGCGGCGATCATCTGACCGCGCAAG 1383  
DB 1279 CCAACCAAGAGGCGCATCAAGTACCAAGAGCGGCGATCATCTGACCGCGCAAG 1338  
QY 1384 CCGGCAAGCGCGGCGGCTGAGCGGCTGAGCGGCTGAGATGATCCAGAACCGATGAGC 1443  
DB 1339 CCGGCAAGCGCGGCGGCTGAGCGGCTGAGCGGCTGAGATGATCCAGAACCGATGAGC 1398  
QY 1444 TGAAGTGAATCTGCGAGAGAGTTCGCAAGAGTGAAGCGGCTCATTAAGAGATCTACG 1503  
DB 1399 TGAAGTGAATCTGCGAGAGAGTTCGCAAGAGTGAAGCGGCTCATTAAGAGATCTACG 1458  
QY 1504 ACTCCGCGATGAGGCGGCTCCCGAGATTAAGTGAATGAGTGAATGAGGCGGCGCAATCG 1563  
DB 1459 ACTCCGCGATGAGGCGGCTCCCGAGATTAAGTGAATGAGTGAATGAGGCGGCGCAATCG 1518  
QY 1564 CCGGCTTCAACCAAGTGGCTGATGCTCCGTAAGGCGGCGGCTGTTAAAGCTGCGCAG 1623  
DB 1519 CCGGCTTCAACCAAGTGGCTGATGCTCCGTAAGGCGGCGGCTGTTAAAGCTGCGCAG 1578  
QY 1624 CCAAGCGAAGGCTCAACCGGCAATCAACCAACCACTCAAGGCGGCGGAGCTTTCG 1683  
DB 1579 CCAAGCGAAGGCTCAACCGGCAATCAACCAACCACTCAAGGCGGCGGAGCTTTCG 1638  
QY 1684 AAGCGGCGGCTTTCGAGCGAGGCGCTCACTGCGCTTTCATTAAGCTGCTATTCG 1743  
DB 1639 AAGCGGCGGCTTTCGAGCGAGGCGCTCACTGCGCTTTCATTAAGCTGCTATTCG 1688  
QY 1744 GCGTGGCGGCTGCAATTCACCCCAAGAAAGCTAGGCGGCACTGATCAGAGCG 1803  
DB 1699 GCGTGGCGGCTGCAATTCACCCCAAGAAAGCTAGGCGGCACTGATCAGAGCG 1758  
QY 1804 CTATTTTTCGCGAGCGGCGCTCAACCGGAGGCTCTTCCCGGAGGCTTAAAGGCT 1863  
DB 1759 CTATTTTTCGCGAGCGGCGCTCAACCGGAGGCTCTTCCCGGAGGCTTAAAGGCT 1818  
QY 1864 GAGGTGCGGCGGACTTTCGCGGAGCATGCGTGGTTTGAAGCGGCTCAAGTCAAGCAG 1923  
DB 1819 GAGGTGCGGCGGACTTTCGCGGAGCATGCGTGGTTTGAAGCGGCTCAAGTCAAGCAG 1878



QY	901	ACGGGCGCGTCTGTTTGTGGAAACGTCGTAAGAGACAAAGGGGAGAGGCTCAAGGGCA	960
Db	901	ACGGGCGCGTCTGTTTGTGGAAACGTCGTAAGAGACAAAGGGGAGAGGCTCAAGGGCA	960
QY	961	AGCGCTGCTGTGTCTGCGCGGGCAACGTGGCCAGTACTGCGCGAGCTGCTGTGG	1020
Db	961	AGCGCTGCTGTGTCTGCGCGGGCAACGTGGCCAGTACTGCGCGAGCTGCTGTGG	1020
QY	1021	AGAAAGGCGCCATGTGTGTGTGCTGTCCGACTCCAGGGCTTACGTGTACGAGCCCAACG	1080
Db	1021	AGAAAGGCGCCATGTGTGTGTGCTGTCCGACTCCAGGGCTTACGTGTACGAGCCCAACG	1080
QY	1081	GCTTCAGCGGGACAGCTGACGGCGGTGACAGACATGANAANAAGAAACAAGCGGCC	1140
Db	1081	GCTTCAGCGGGACAGCTGACGGCGGTGACAGACATGANAANAAGAAACAAGCGGCC	1140
QY	1141	GCACTCTCGAATACAAAGACGACACCGCCGTTATGTGTGGGAGACCGCGCAAGCCTTGGG	1200
Db	1141	GCACTCTCGAATACAAAGACGACACCGCCGTTATGTGTGGGAGACCGCGCAAGCCTTGGG	1200
QY	1201	AGCTGAGCTGCGCAGGTGACATCGCTTTCCCTGTGCGCCACCCAGAACGAGATCGATGAGC	1260
Db	1201	AGCTGAGCTGCGCAGGTGACATCGCTTTCCCTGTGCGCCACCCAGAACGAGATCGATGAGC	1260
QY	1261	ACGACGCCGAGACTCTGATCAAGACACGGCTGCCAGTACGTGTGTAAGAGGGCGCCAAATGC	1320
Db	1261	ACGACGCCGAGACTCTGATCAAGACACGGCTGCCAGTACGTGTGTAAGAGGGCGCCAAATGC	1320
QY	1321	CCTCCACCAAGAGAGCCATCCACAAGTATCAACAAGGCGGATCATCTACGCCCGGCA	1380
Db	1321	CCTCCACCAAGAGAGCCATCCACAAGTATCAACAAGGCGGATCATCTACGCCCGGCA	1380
QY	1381	AGGCGGCCCAACGCGCGCGCGCTGCGGTCAAGCGGCTGTGAGATGACCCAGAACCGCATGA	1440
Db	1381	AGGCGGCCCAACGCGCGCGCGCTGCGGTCAAGCGGCTGTGAGATGACCCAGAACCGCATGA	1440
QY	1441	GCCGTGAATGTGAACCTGCGAGAGAGGTTCGCGACAAGCTGGAACCGATATGAAGAACAATCT	1500
Db	1441	GCCGTGAATGTGAACCTGCGAGAGAGGTTCGCGACAAGCTGGAACCGATATGAAGAACAATCT	1500
QY	1501	ACGACTCCGCGATGGGGCGCTCCGAGATACAAATGTTGACCTGAGCTGGGGCGCCACA	1560
Db	1501	ACGACTCCGCGATGGGGCGCTCCGAGATACAAATGTTGACCTGAGCTGGGGCGCCACA	1560
QY	1561	TCGCGGGGCTTACCAAGGTGCTGATGCGGTCAAGGCCAGGGCGCTGTTTAACTGCGCC	1620
Db	1561	TCGCGGGGCTTACCAAGGTGCTGATGCGGTCAAGGCCAGGGCGCTGTTTAACTGCGCC	1620
QY	1621	AGGCCCAAGCCACGGCTTACCGGCAATCAACCAACATCTCAACGGCCAGGACCTTTT	1680
Db	1621	AGGCCCAAGCCACGGCTTACCGGCAATCAACCAACATCTCAACGGCCAGGACCTTTT	1680
QY	1681	CGAAGAGCGGCGCTTTTCCGAGCCAGGGGCGCTCACTGCGCTTTCATTAACCTGCTATT	1740
Db	1681	CGAAGAGCGGCGCTTTTCCGAGCCAGGGGCGCTCACTGCGCTTTCATTAACCTGCTATT	1740
QY	1741	GCCGCGGTGCCCTGTCAATTCACCCCAAGAAAGCTTAGCGGCACTTGACTGATCAAGA	1800
Db	1741	GCCGCGGTGCCCTGTCAATTCACCCCAAGAAAGCTTAGCGGCACTTGACTGATCAAGA	1800
QY	1801	CGGCTATTTTTTTGGCGACGGCGCTCACCCCGAGAGGCTCTCTCCCGGAGCCCTTAAGC	1860
Db	1801	CGGCTATTTTTTTGGCGACGGCGCTCACCCCGAGAGGCTCTCTCCCGGAGCCCTTAAGC	1860
QY	1861	GCTACGTCGCGCCGCACTTGGCTGTGCAATGCGCTCGGTTTTGAACCCCTCAAGTACAC	1920
Db	1861	GCTACGTCGCGCCGCACTTGGCTGTGCAATGCGCTCGGTTTTGAACCCCTCAAGTACAC	1920
QY	1921	CACCTGTGTGAAGCCTACAGGCTCAATGCTTTTATGTATGTGCGCCCGCTCTGAC	1980
Db	1921	CACCTGTGTGAAGCCT--CAGCTCAATGCTCTTTTATGTATGTGCGCCCGCTCTGAC	1970
QY	1981	CCCCGAATTTTCTGTCCATGAGACGTGCGGTTCTTAAGCTGTGATACCCCAAGTACAGTT	2040

DB	1971	CCCCGAATTTTCC	TCCGCA--	AGAGTGGGTTCTTACCTGGTGA	CCCCCAAGTAGCAGTT	2028
Qy	2041	AGTGTGGTGCCTTGGCTTGGCTGGCTGGCCCGGAGTGC	GAATCTGTGACCTGAGAGTGC	TTGT	2100	
Db	2029	AGTGTGGTGCCTTGGCTTGGCTGGCC--CGCTGCCCGGATGC	GAATCTGTGACCTGAGAGTGC	TTGT	2086	
Qy	2101	GTAAACACGACGAGTCA	AAAAAAAAAAAAAAAAAAAA	2138		
Db	2087	GTAAACACGACGAGTCA	AAAAAAAAAAAAAAAAAAAA	2124		
RESULT 10						
AT64531	ID	AAT64531 standard; cDNA; 1969 BP.				
XX	AC	AAT64531;				
XX	DT	17-OCT-2003 (reviewed)				
DT	DT	10-JUL-1997 (first entry)				
XX	DE	Glutamate dehydrogenase cDNA clone pBGdc53.				
XX	KW	Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;				
XX	KX	chloroplast; transgenic plant; de.				
OS	XX	Chlorella sorokiniana, strain UTEX 1230.				
XX	PN	W09712983-A1.				
XX	PD	10-APR-1997.				
XX	PF	03-OCT-1996; 96WO-US015921.				
XX	PR	06-OCT-1995; 95US-00541033.				
XX	PA	(UFL) UNIV FLORIDA.				
P1	XX	Schmidt RR, Miller P;				
DR	XX	WPI; 1997-226226/20.				
PT	XX	DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella				
PT	XX	sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism				
PS	XX	plant cells.				
PS	XX	Claim 2; Page 35-36; 61pp; English.				
CC	XX	A cDNA clone (AAT64531), designated pBGdc53, was isolated from a				
CC	XX	Chlorella sorokiniana cDNA library in lambda ZAP by screening with an				
CC	XX	NADP-specific glutamate dehydrogenase (NADP-GDH) cDNA probe. It comprises				
CC	XX	the complete 3'-terminal region of the C. sorokiniana NADP-GDH sequence.				
CC	XX	5' terminal regions were obt. by PCR, yielding full-length clones				
CC	XX	(AAT64542-43) for the alpha and beta subunits of C. sorokiniana NADP-GDH.				
CC	XX	(Updated on 17-OCT-2003 to standardise OS field)				
SO	XX	Sequence 1969 BP; 401 A; 659 C; 580 G; 329 T; 0 U; 0 Other;				
Qy	Match	92.0%; Score 1969; DB 2; Length 1969;				
Qy	Best Local Similarity	100.0%; Pred. No. 0;				
Qy	Matches 1969; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
Db	1	CAGATCTCCGCGATGACGCCACCGCGGACTTCA	CGGCGCTGCAGAAAGCGGTGAAG	230		
Qy	231	CAGATGGCCACCAAGCGGGCACTGAGGGCTTGGTGC	ACGGCATCAAGAACCCGACGTG	290		
Db	61	CAGATGGCCACCAAGCGGGCACTGAGGGCTTGGTGC	ACGGCATCAAGAACCCGACGTG	120		
Qy	291	CGCAGCTGCTGACCGAGATCTTATAGAGACCCGAGACGACGAGATTCATGACAGCG	350			
Db	121	CGCAGCTGCTGACCGAGATCTTATAGAGACCCGAGACGACGAGATTCATGACAGCG	180			



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QY 351 GTGGCGAGGTGGCCGTCCTCCCTGCAAGCCGCTGTTCAGAAAGCGCCCGAGCTGTGCCC 410
DB 181 GTGGCGAGGTGGCCGTCCTCCCTGCAAGCCGCTGTTCAGAAAGCGCCCGAGCTGTGCCC 240
QY 411 ATCTTCAAGAGATGTTGAGCGCTGAGCGCGTGATCACTTCCGCGTGTCTGCTGAGC 470
DB 241 ATCTTCAAGAGATGTTGAGCGCGTGATCACTTCCGCGTGTCTGCTGAGC 300
QY 471 GAGCCGCGCAACCTGCAAGTCAACCGCGCGCTTCCGCGTGAGTACTGTCGCGCATCCGC 530
DB 301 GAGCGCGCAACCTGCAAGTCAACCGCGCGCTTCCGCGTGAGTACTGTCGCGCATCCGC 360
QY 531 CCCTTCAAGAGCGCGCTGCTGCTTCCAGCCCTCCGGAACCTGTCCATGATGAATTCCTT 590
DB 361 CCCTTCAAGAGCGCGCTGCTGCTTCCAGCCCTCCGGAACCTGTCCATGATGAATTCCTT 420
QY 591 GCCTTTGAGAGATCTTCAAGAACAGCTGACCACTGCGCATGAGCGCGCGCAAGGCG 650
DB 421 GCCTTTGAGAGATCTTCAAGAACAGCTGACCACTGCGCATGAGCGCGCGCAAGGCG 480
QY 651 GGCCTCCGACTTTCGACCCCAAGGCGCAAGAGCGAGCGAGTGATGCGCTTCTGCCAGTCC 710
DB 481 GGCCTCCGACTTTCGACCCCAAGGCGCAAGAGCGAGCGAGTGATGCGCTTCTGCCAGTCC 540
QY 711 TTCAATGACCGAGCTGCAAGCGCAATCAAGCTGAGAGACGTCGCGCGCGCGCAATC 770
DB 541 TTCAATGACCGAGCTGCAAGCGCAATCAAGCTGAGAGACGTCGCGCGCGCGCAATC 600
QY 771 GGCCTGAGCGCGCGCGAGATTTGCTACTTTCGCGCATGACCAAGCGCATCAACAGAAC 830
DB 601 GGCCTGAGCGCGCGCGAGATTTGCTACTTTCGCGCATGACCAAGCGCATCAACAGAAC 660
QY 831 TACACCGGCGTGTGACCCCGAAGGCGCAAGAGTATGCGCGCTCCGAGATCCGCCGAG 890
DB 661 TACACCGGCGTGTGACCCCGAAGGCGCAAGAGTATGCGCGCTCCGAGATCCGCCGAG 720
QY 891 GGCACCGGCTACCGGCGCGCTGTGTTGTTGAGAAACGTCGTAAGAGAACAGGCGAGAGC 950
DB 721 GGCACCGGCTACCGGCGCGCTGTGTTGTTGAGAAACGTCGTAAGAGAACAGGCGAGAGC 780
QY 951 CTCAAGGCGCAAGCGCTGCTGTGTCTGCGCGCGCAACGTGCGCCAGTACTGCGCGAG 1010
DB 781 CTCAAGGCGCAAGCGCTGCTGTGTCTGCGCGCGCAACGTGCGCCAGTACTGCGCGAG 840
QY 1011 CTGCTGCTGAGAAAGGCGCGCATGTGTCTGTCTGCTGCACTCCAGGCGCTACGCTTAC 1070
DB 841 CTGCTGCTGAGAAAGGCGCGCATGTGTCTGTCTGCTGCACTCCAGGCGCTACGCTTAC 900
QY 1071 GAGGCCCAACCGGCTTCAAGCGCGAGAGAGTGAAGCGCGTGAGACATGAAGAAGAAC 1130
DB 901 GAGGCCCAACCGGCTTCAAGCGCGAGAGAGTGAAGCGCGTGAGACATGAAGAAGAAC 960
QY 1131 AACAGCGCGCGCATCTCGAGATCAAGAGCAACCGCGCTGTATGTGGCGACCGCGCG 1190
DB 961 AACAGCGCGCGCATCTCGAGATCAAGAGCAACCGCGCTGTATGTGGCGACCGCGCG 1020
QY 1191 AAGCTTTGAGAGCTGAGCTGCAAGTGAATCGCTTTCCTGCGCCACCAAGACGAG 1250
DB 1021 AAGCTTTGAGAGCTGAGCTGCAAGTGAATCGCTTTCCTGCGCCACCAAGACGAG 1080
QY 1251 ATCGATGAGCAAGAGCGCGAGCTGTATCAAGCAACCGCTGCAAGTATGTGTGAGGAGC 1310
DB 1081 ATCGATGAGCAAGAGCGCGAGCTGTATCAAGCAACCGCTGCAAGTATGTGTGAGGAGC 1140
QY 1311 GCGAATGATGCTCTCAACCAAGAGCGCATCAAGATCAAGCAAGAGCGCGCATCACTAC 1370
DB 1141 GCGAATGATGCTCTCAACCAAGAGCGCATCAAGATCAAGCAAGAGCGCGCATCACTAC 1200
QY 1371 TGCCCGGCAAGAGCGCGCAACGCGCGCGCGTGGCGATCAAGCGCGCTGAGATGACCCAG 1430
DB 1201 TGCCCGGCAAGAGCGCGCAACGCGCGCGCGTGGCGATCAAGCGCGCTGAGATGACCCAG 1260

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QY 1431 AACCGATGAGCTGAACTGCACTCGGAGAGAGTTCGCGCAAGAGCTGAGCGCATATG 1490
DB 1261 AACCGATGAGCTGAACTGCACTCGGAGAGAGTTCGCGCAAGAGCTGAGCGCATATG 1320
QY 1491 AAGGACATCTACGACTCGCGCATGAGGCGCGTCCGCGAGATACAAATGTTGACTTGCTGCG 1550
DB 1321 AAGGACATCTACGACTCGCGCATGAGGCGCGTCCGCGAGATACAAATGTTGACTTGCTGCG 1380
QY 1551 GGGCGCAACATCGGCGGCTTCAACAGTGTGTATGCGCGCATGCGCGCGCGCGCTGTT 1610
DB 1381 GGGCGCAACATCGGCGGCTTCAACAGTGTGTATGCGCGCATGCGCGCGCGCGCTGTT 1440
QY 1611 TAACTGCGCGAGCGCCCAAGCGCATCAACCGGAGATCAACCAACCACTCAACGCGCC 1670
DB 1441 TAACTGCGCGAGCGCCCAAGCGCATCAACCGGAGATCAACCAACCACTCAACGCGCC 1500
QY 1671 AGAACCTTTTCGAAAGCGCGCGCTTTTTCAGGCGAGGCGCTCACTGCGCTTTCATTA 1730
DB 1501 AGAACCTTTTCGAAAGCGCGCGCTTTTTCAGGCGAGGCGCTCACTGCGCTTTCATTA 1560
QY 1731 CCTGCTATTTGCGCGCGCTGCGCTGCAATTCACCCCAAGAGAACTAGCGGCACTTGAC 1790
DB 1561 CCTGCTATTTGCGCGCGCTGCGCTGCAATTCACCCCAAGAGAACTAGCGGCACTTGAC 1620
QY 1791 TGCAATCAAGAGCGCTATTTTTCGCGAGCGCGCTCAACCCCGAGAGCGCTCTCCCGCG 1850
DB 1621 TGCAATCAAGAGCGCTATTTTTCGCGAGCGCGCTCAACCCCGAGAGCGCTCTCTCCCGCG 1680
QY 1851 AGCCCTAAGCGCTGACGCTGCGCGCGCTTTCGCAATGCTGCGTCTTTCATTA 1910
DB 1681 AGCCCTAAGCGCTGACGCTGCGCGCGCTTTCGCAATGCTGCGTCTTTCATTA 1740
QY 1911 CCACTTACCCCAACCTGTTGTTGAAAGCTTACCAAGCTCAATTCCTTTTATGTTAGTGGC 1970
DB 1741 CCACTTACCCCAACCTGTTGTTGAAAGCTTACCAAGCTCAATTCCTTTTATGTTAGTGGC 1800
QY 1971 CCCCTCGCGCGCGCGAAATTTTCTGTCATGAGAGAGTGGCGTCTTACGCTGTGAGCCCA 2030
DB 1801 CCCCTCGCGCGCGCGAAATTTTCTGTCATGAGAGAGTGGCGTCTTACGCTGTGAGCCCA 1860
QY 2031 AGTAGAGTATGTTGCTGCTGCTTTCCTGCGCTGCGCGCGATGCGATCTGTGACCTGA 2090
DB 1861 AGTAGAGTATGTTGCTGCTGCTTTCCTGCGCTGCGCGCGATGCGATCTGTGACCTGA 1920
QY 2091 GAGTCTTGTGTAAACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2139
DB 1921 GAGTCTTGTGTAAACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 1969

RESULT 11
ABK51009
ID ABK51009 standard; cDNA; 1969 BP.
XX
XX ABK51009;
AC
XX
XX 24-SEP-2002 (first entry)
DT
XX
XX NADP-glutamate dehydrogenase clone pBGdc53.
DE
XX
XX NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
KW ammonia toxicity tolerance; osmotic stress tolerance; pBGdc53; gene; ss.
OS Chlorella sorokiniana.
XX
XX US2002062495-A1.
XX
XX 23-MAY-2002.
XX
XX 01-MAY-1998; 98US-00070844.
XX
XX 01-MAY-1998; 98US-00070844.
XX
XX

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PA (SCHM/) SCHMIDT R. R.  
PA (MILL/) MILLER P.  
PI Schmidt RR, Miller P;  
XX WPI; 2002-499691/53.  
XX  
XX Transforming a plant with a polynucleotide encoding a polypeptide with  
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen  
PT metabolism useful to increase yield and ammonium and osmotic stress  
PT tolerance.  
XX  
XX Example 2; Page 19-20; 35pp; English.  
XX  
XX The invention relates to a method of modulating nitrogen metabolism in  
CC plant cells, comprising transforming a plant cell with a polynucleotide  
CC encoding a polypeptide having glutamate dehydrogenase activity, and  
CC culturing the cell to produce descendant cells which express the  
CC polypeptide. The method is used to provide plants with increased yield,  
CC improved ammonium assimilation properties, increased tolerance to ammonia  
CC toxicity, improved osmotic stress tolerance and improved composition. The  
CC present sequence represents the coding sequence of Chlorella sorokiniana  
CC NADP-glutamate dehydrogenase clone p8Dc53, used in the method of the  
CC invention  
SQ Sequence 1969 BP; 401 A; 659 C; 580 G; 329 T; 0 U; 0 Other;  
Query Match 92.0%; Score 1969; DB 6; Length 1969;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 171 CAGATCTCCGAGTGAAGCCACCGCGCATTTCAAGCGCTGACAGAGCGGTGAAG 230  
DB 1 CAGATCTCCGAGTGAAGCCACCGCGCATTTCAAGCGCTGACAGAGCGGTGAAG 60  
QY 231 CAGATGCGCACCAAGCGCGGCACTGAGGGCTGTGTGCAAGCGATCAAGAACCCCGACGTG 290  
DB 61 CAGATGCGCACCAAGCGCGGCACTGAGGGCTGTGTGCAAGCGATCAAGAACCCCGACGTG 120  
QY 291 CGCCAGCTGTGACCGGAGATCTTCAATGAAGACCGCGAGCAGAGAGTTGATGACAGCG 350  
DB 121 CGCCAGCTGTGACCGGAGATCTTCAATGAAGACCGCGAGCAGAGAGTTGATGACAGCG 180  
QY 351 GTGCGCGAGGTGCGCTCTCCCTGACGCGGTGTGAGAGAGCGGCCGAGCTGTGCGC 410  
DB 181 GTGCGCGAGGTGCGCTCTCCCTGACGCGGTGTGAGAGAGCGGCCGAGCTGTGCGC 240  
QY 411 ATCTTCAAGAGATGTTGAGCTTGAGCGCGGTGATCACCTTCCGCGTCTGTGCTGAGC 470  
DB 241 ATCTTCAAGAGATGTTGAGCTTGAGCGCGGTGATCACCTTCCGCGTCTGTGCTGAGC 300  
QY 471 GACCGCGGCAACCTGACAGGTCAACCGCGGCTTCCCGGTGACGTAATCTCTCCGCAATCGGC 530  
DB 301 GACCGCGGCAACCTGACAGGTCAACCGCGGCTTCCCGGTGACGTAATCTCTCCGCAATCGGC 360  
QY 531 CCTTCAAGAGGCGGCTGCTTCCACCCCTCCGTAACCTGTTCATGATGAAGTTCTT 590  
DB 361 CCTTCAAGAGGCGGCTGCTTCCACCCCTCCGTAACCTGTTCATGATGAAGTTCTT 420  
QY 591 GCTTTGAGCAGATCTTCAAGAACGCTGACCACTTCCATGAGGCGGCGGCAAGGCG 650  
DB 421 GCTTTGAGCAGATCTTCAAGAACGCTGACCACTTCCATGAGGCGGCGGCAAGGCG 480  
QY 651 GCGTCCGACTTGAAGCCCAAGGCAAGAGCGAGCGGAGGTGATGCGCTTGTGCGAGTCC 710  
DB 481 GCGTCCGACTTGAAGCCCAAGGCAAGAGCGAGCGGAGGTGATGCGCTTGTGCGAGTCC 540  
QY 711 TTCAATGACGAGCTGACGCGCAATGAGTGAAGAGAGTGCAGCGCGCGGCGCAATC 770  
DB 541 TTCAATGACGAGCTGACGCGCAATGAGTGAAGAGAGTGCAGCGCGCGGCGCAATC 600  
QY 771 GCGGTGCGCGCGGAGATTGCTACTTTTCCGCGCAGTCAAGCGCATCAAGAGAC 830

DB 601 GCGGTGCGCGCGGAGATTGCTACTTTTCCGCGCAGTCAAGCGCATCAAGAGAAC 660  
QY 831 TACACCGGCGGTGCTGAACCCCGAAGGGCGCAGAGATGAGCGGCTCCAGATCCGCCCGAG 890  
DB 661 TACACCGGCGGTGCTGAACCCCGAAGGGCGCAGAGATGAGCGGCTCCAGATCCGCCCGAG 720  
QY 891 GCCACCGGCTTACCGCGCGGCTGTTTGTGAGAACGTGTGAGAACCAAGGCGAGAGC 950  
DB 721 GCCACCGGCTTACCGCGCGGCTGTTTGTGAGAACGTGTGAGAACCAAGGCGAGAGC 780  
QY 951 CTCAAGGGCAAGCGCTGCTGTGTCTGTGCGCGGCAACGTGGCCCATGTCTCGCGGAG 1010  
DB 781 CTCAAGGGCAAGCGCTGCTGTGTCTGTGCGCGGCAACGTGGCCCATGTCTCGCGGAG 840  
QY 1011 CTGCTGTGAGAGAGGGCGGCGCATGTGTGCTGTGCTGCTCCAGGCTACAGGCTAGTGTAC 1070  
DB 841 CTGCTGTGAGAGAGGGCGGCGCATGTGTGCTGTGCTGCTCCAGGCTACAGGCTAGTGTAC 900  
QY 1071 GAGCCCAACCGGCTTCAAGCGCGGAGCAGCTGAGCGGTGAGGACATGAAGAAAGAAC 1130  
DB 901 GAGCCCAACCGGCTTCAAGCGCGGAGCAGCTGAGCGGTGAGGACATGAAGAAAGAAC 960  
QY 1131 AACAGCGCGGCACTTCCGAGTACAGAGGCAACCGCGGTGTATGTGGCGCACCGCCG 1190  
DB 961 AACAGCGCGGCACTTCCGAGTACAGAGGCAACCGCGGTGTATGTGGCGCACCGCCG 1020  
QY 1191 AAGCTTGGGAGCTGAGCTGCGAGGTGAGATGCGCTTCCCGCGGCGCACCGAAGAG 1250  
DB 1021 AAGCTTGGGAGCTGAGCTGCGAGGTGAGATGCGCTTCCCGCGGCGCACCGAAGAG 1080  
QY 1251 ATCGATGAGCAAGCGCGGAGCTGTGATCAAGCAGCGGCTGCCAGTACGTGTGAGAGG 1310  
DB 1081 ATCGATGAGCAAGCGCGGAGCTGTGATCAAGCAGCGGCTGCCAGTACGTGTGAGAGG 1140  
QY 1311 GCCAATGCGCTTCAACCAAGAGGCTATCCAAGATCAACAAAGCGGCGCATATCTAC 1370  
DB 1141 GCCAATGCGCTTCAACCAAGAGGCTATCCAAGATCAACAAAGCGGCGCATATCTAC 1200  
QY 1371 TGCCCGGCAAGCGGCGCAACCGCGGCGGTGTGAGCGGCTGTGAGATGACCCAG 1430  
DB 1201 TGCCCGGCAAGCGGCGCAACCGCGGCGGTGTGAGCGGCTGTGAGATGACCCAG 1260  
QY 1431 AACCGATGAGCTGAACTGGAATCGGAGAGAGTTGCGCAACAAAGCTGAGCGCATATG 1490  
DB 1261 AACCGATGAGCTGAACTGGAATCGGAGAGAGTTGCGCAACAAAGCTGAGCGCATATG 1320  
QY 1491 AAGGACCTTACGACTCCGCAATGAGGCGCTCCCGGAGATACAAATGTGACCTGGCTGCG 1550  
DB 1321 AAGGACCTTACGACTCCGCAATGAGGCGCTCCCGGAGATACAAATGTGACCTGGCTGCG 1380  
QY 1551 GCGCGCAACATCGCGGCTTCAACCAAGTGTGATGCGTCAAGGCGGCGGCGCTGTT 1610  
DB 1381 GCGCGCAACATCGCGGCTTCAACCAAGTGTGATGCGTCAAGGCGGCGGCGCTGTT 1440  
QY 1611 TAAAGCTCCCAAGGCGGCGCAAGCGCTCACCGGCAATCAACCCCAACCACTCAACGCGC 1670  
DB 1441 TAAAGCTCCCAAGGCGGCGCAAGCGCTCACCGGCAATCAACCCCAACCACTCAACGCGC 1500  
QY 1671 AAGACCTTTTGGAGAGCGGCGCTTTTCCAGCAGAGGCGCTCACTGCGCTTCAATA 1730  
DB 1501 AAGACCTTTTGGAGAGCGGCGCTTTTCCAGCAGAGGCGCTCACTGCGCTTCAATA 1560  
QY 1731 CCGTCTATTGCGCGCGTGCCTTCAATTCACCCCAAGAAAGAACTAGGCGCATTTGAC 1790  
DB 1561 CCGTCTATTGCGCGCGTGCCTTCAATTCACCCCAAGAAAGAACTAGGCGCATTTGAC 1620  
QY 1791 TGCAATGAGAGCGGCTATTTTGTGCGAGCGCGCTCAACCCGAGAGCTCTCTCCCGG 1850  
DB 1621 TGCAATGAGAGCGGCTATTTTGTGCGAGCGCGCTCAACCCGAGAGCTCTCTCCCGG 1680  
QY 1851 AGCCCTAAGGCGTGAAGTCCGCGGAGCTTTGCTCGCATGTGCTGTTTGAACCCCT 1910  
DB 1681 AGCCCTAAGGCGTGAAGTCCGCGGAGCTTTGCTCGCATGTGCTGTTTGAACCCCT 1740

QY 1911 CCAAGTCTACCCACCTGTGTGTAAGCTACAGCTCAATTCCTTTAGTATGAGGC 1970  
 DB 1741 CCAAGTCTACCCACCTGTGTGTAAGCTACAGCTCAATTCCTTTAGTATGAGGC 1800  
 QY 1971 CCCCTCTGCCCCCGAAATTTTCTCTGCAATGAGACGTGGGTTCTAGCTGTGACCCA 2030  
 DB 1801 CCCCTCTGCCCCCGAAATTTTCTCTGCAATGAGACGTGGGTTCTAGCTGTGACCCA 1860  
 QY 2031 AGTAGCAATGATGTGCTGCTTCCCTGCGCTGCGCGGATGCGATCTGTACCTGA 2090  
 DB 1861 AGTAGCAATGATGTGCTGCTTCCCTGCGCTGCGCGGATGCGATCTGTACCTGA 1920  
 QY 2091 GAGTCTGTGTAAACAGACGAGTCAAAAAA 2139  
 DB 1921 GAGTCTGTGTAAACAGACGAGTCAAAAAA 1969  
 RESULT 12  
 ADQ36708  
 ID ADQ36708 standard; cDNA; 2083 BP.  
 AC ADQ36708;  
 XX 23-SEP-2004 (first entry)  
 DE NADP-specific GDH beta subunit precursor protein cDNA, SEQ ID 3.  
 XX NADP-specific GDH beta subunit precursor protein cDNA, SEQ ID 3.  
 XX Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;  
 KM beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase;  
 KW gene; ss.  
 XX Chlorella sorokiniana.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 33..1571  
 FT /tag= a  
 FT /product= "NADP-specific GDH beta subunit precursor  
 FT protein"  
 XX US2004128710-A1.  
 XX 01-JUL-2004.  
 PD 24-JUL-2003; 2003US-00627886.  
 XX 01-MAY-1998; 98US-00070844.  
 PR (SCHMIDT R R.  
 PA (MILLER P.  
 PA (MILLER P.  
 PI Schmidt RR, Miller P,  
 XX WPI: 2004-533134/51.  
 DR P-PSDB; ADQ36709.  
 XX  
 PT Increasing or decreasing nitrogen metabolism in plant cells, for plant  
 PT with increased yield and improved tolerance to ammonia toxicity and  
 PT osmotic stress, by transforming plant cell with nucleic acid having  
 PT glutamate dehydrogenase activity.  
 XX  
 PS Disclosure; SEQ ID NO 3; 36pp; English.  
 XX  
 CC The present invention relates to increasing or decreasing the nitrogen  
 CC metabolism in plant cells by transforming a plant cell with a  
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase  
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,  
 CC ADQ36731), or their fragments, which exhibits GDH activity. The  
 CC polynucleotide is operably linked to a polynucleotide encoding a  
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their  
 CC fragments that exhibit chloroplast transit activity. The method is useful  
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The

CC methods, polynucleotides, and polypeptides are useful in producing plant  
 CC with increased yield, and with improved tolerance to ammonia toxicity,  
 CC osmotic stress, and composition of the crop or plant. The present  
 CC sequence is the coding sequence for the precursor protein of the beta  
 CC subunit of the NADP-specific GDH, which is then processed to produce the  
 CC mature alpha subunit of the NADP-specific GDH, used in the method of the  
 CC invention.  
 SQ Sequence 2083 BP; 415 A; 709 C; 611 G; 348 T; 0 U; 0 Other;  
 Query Match 90.5%; Score 1935.8; DB 12; Length 2083;  
 Best Local Similarity 97.1%; Pred. No. 1e-310;  
 Matches 2076; Conservative 0; Mismatches 7; Indels 56; Gaps 8;  
 QY 1 CTCCTTTTGTGCTGCGCCCTCTCTCCGTCATGACAGACCGCCCTGTGCCCAAGCTTA 60  
 DB 1 CTCCTTTTGTGCTGCGCCCTCTCTCCGTCATGACAGACCGCCCTGTGCCCAAGCTTA 60  
 QY 61 TCGTGGCCGCCCGCTGGCGGACAGCCCGGCTGCTGCGCGTGGCCGCTGGG 120  
 DB 61 TCGTGGCC-----TGGCGTGGG 78  
 QY 121 TCGGCTCGCCAGCGCGATGTCGCGCAAGCGCTGCTGCTGAGAGAGATCTTCG 180  
 DB 79 TCGGCTCGCCAGCGCGATGTCGCGCAAGCGCTGCTGCTGAGAGAGATCTTCG 138  
 QY 181 CGATGAGACGCCACACCGCGGACCTTTCAGCGGCTGCGAGAGGCGGTGAAGATGGCCA 240  
 DB 139 CGATGAGACGCCACACCGCGGACCTTTCAGCGGCTGCGAGAGGCGGTGAAGATGGCCA 198  
 QY 241 CCAAGCGCGGACCTGAGGCGCTGTCAGCGGCATCAAGAACCCGACGTGCGCCAGCTGC 300  
 DB 199 CCAAGCGCGGACCTGAGGCGCTGTCAGCGGCATCAAGAACCCGACGTGCGCCAGCTGC 258  
 QY 301 TGACGAGATCTTATGAGAGACCGGAGACGAGAGTTCATGACGCGGTGGCCGAG 360  
 DB 259 TGACGAGATCTTATGAGAGACCGGAGAGGAGGATTCATGACGCGGTGGCCGAG 318  
 QY 361 TGGCGGCTCTCCCTGACGCGGCTGTCAGAGAGCGCCGAGAGTCTGCTTCAAGC 420  
 DB 319 TGGCGGCTCTCCCTGACGCGGCTGTCAGAGAGCGCCGAGAGTCTGCTTCAAGC 378  
 QY 421 AGATCGTTGAGCGTGAAGCGGCTGATCACTCCGCGTCTGCTGCTGAGAGACCGCGCA 480  
 DB 379 AGATCGTTGAGCGTGAAGCGGCTGATCACTCCGCGTCTGCTGCTGAGAGACCGCGCA 438  
 QY 481 ACCTGACAGTCAACCGCGGCTTCCGCTGAGTACTGCTCCGCAATGAGGCCCTTACAAG 540  
 DB 439 ACCTGACAGTCAACCGCGGCTTCCGCTGAGTACTGCTCCGCAATGAGGCCCTTACAAG 498  
 QY 541 GCGGCTGCGCTTCCACCCCTCCGTAACCTGTCCATCATGAAGTTCCTTGCCTTGAAGC 600  
 DB 499 GCGGCTGCGCTTCCACCCCTCCGTAACCTGTCCATCATGAAGTTCCTTGCCTTGAAGC 558  
 QY 601 AGATCTTCAAGAACAGCTGACCAACCTGCGCAATGAGCGGCGCAAGGCGGCTCCGACT 660  
 DB 559 AGATCTTCAAGAACAGCTGACCAACCTGCGCAATGAGCGGCGCAAGGCGGCTCCGACT 618  
 QY 661 TCGACCCCAAGGAGGAGGAGGAGCGAGAGTATGAGCTTCTGCAATCTTCAAGACG 720  
 DB 619 TCGACCCCAAGGAGGAGGAGGAGGAGGAGTATGAGCTTCTGCAATCTTCAAGACG 678  
 QY 721 AGCTGACGCGCACATGACTGACGAGAGTGCCTGCGCGGAGCAATGCGCTTGAAGC 780  
 DB 679 AGCTGACGCGCACATGACTGACGAGAGTGCCTGCGCGGAGCAATGCGCTTGAAGC 738  
 QY 781 CCGCGGAGATTTGCTACTTTTGGGCGAGTCAAGAGGATCAACCAAGATCAACCGGCG 840  
 DB 739 CCGCGGAGATTTGCTACTTTTGGGCGAGTCAAGAGGATCAACCAAGATCAACCGGCG 798  
 QY 841 TGCTGACCCGGAAGGAGGAGGAGGAGTATGAGGCTTCCGATCCGCGCGAGGACCAAGCT 900  
 DB 799 TGCTGACCCGGAAGGAGGAGGAGGAGTATGAGGCTTCCGATCCGCGCGAGGACCAAGCT 858

OY	901	GGGCGCGCTGCTCTTTTCTGGAGAACGTCGTGAAGAGAACAAAGGCGAGAGCCTCAAGGCGCA	960
Db	859	ACGGCGCGCTGTCTGTTTGTGGAGAACGTGTGTAAGAGAACAAAGGCGAGAGCCTCAAGGCGCA	918
OY	961	AGCGCTGCTGTGTGTCTGGCGCGGGCAACGTGGCCCAAGTACTGGCGCGAGCTGTGTCTGG	1020
Db	919	AGCGCTGCTGTGTGTCTGGCGCGGGCAACGTGGCCCAAGTACTGGCGCGAGCTGTGTCTGG	978
OY	1021	AGAAAGGCGCCATGCTGTCTGTTCCTGTTCGACTCCCAAGGCTTACTGTATCGAGGCCAACG	1080
Db	979	AGAAAGGCGCCATGCTGTCTGTTCCTGTTCGACTCCCAAGGCTTACTGTATCGAGGCCAACG	1038
OY	1081	GCTTCAACGCGAGAGCTGCGAGGCGGGTGCAGAGCATCAAGAAAGAAACAACAGCGGCC	1140
Db	1039	GCTTCAACGCGCGAGAGCTGCGAGGCGGGTGCAGAGCATCAAGAAAGAAACAACAGCGGCC	1098
OY	1141	GCATCTCCGAGTACAAAGAGCCACACCGCGGTGTATGTGGCGAGCCGCGCCAGCCTTGGG	1200
Db	1099	GCATCTCCGAGTACAAAGAGCCACACCGCGGTGTATGTGGCGAGCCGCGCCAGCCTTGGG	1158
OY	1201	AGCTGGAATGCGAAGGTGGACATTCGCTTCCCCTGGGCCACCGAAGAGATTCGATGAGC	1266
Db	1159	AGCTGGAATGCGAAGGTGGACATTCGCTTCCCCTGGGCCACCGAAGAGATTCGATGAGC	1218
OY	1261	ACGACGCGGAGCTGTGATTCAAAGCACGCGCTGCCAGTACGTGTGGAGGGCGCCCAACATGC	1320
Db	1219	ACGACGCGGAGCTGTGATTCAAAGCACGCGCTGCCAGTACGTGTGGAGGGCGCCCAACATGC	1278
OY	1321	CCTCCACCAAGAGAGCCCATCCACAAAGTACAAAGGCGCGCATCATCTACTGCCCGGCA	1380
Db	1279	CCTCCACCAAGAGAGCCCATCCACAAAGTACAAAGGCGCGCATCATCTACTGCCCGGCA	1338
OY	1381	AGGCGGCGCAACGCGCGCGCGGTGGCGGTGACGCGGCTGAGATGACCCAGAACCGCATGA	1440
Db	1339	AGGCGGCGCAACGCGCGCGCGGTGGCGGTGACGCGGCTGAGATGACCCAGAACCGCATGA	1398
OY	1441	GCTTGAACCTGCACTTCGCGAGGAGGTTGCGGACAAAGCTGAGCGCATCATGAGAACATCT	1500
Db	1399	GCTTGAACCTGCACTTCGCGAGGAGGTTGCGGACAAAGCTGAGCGCATCATGAGAGGACATCT	1458
OY	1501	ACGACTCCGCAATGGGGGGCGGTCCGCGACATACATGTTGACTCGGCTGCGGGCGCCAAAC	1560
Db	1459	ACGACTCCGCAATGGGGGGCGGTCCGCGACATACATGTTGACTCGGCTGCGGGCGCCAAAC	1518
OY	1561	TCGCGGGCTTACCAAGGTGGCTGATGCGGTCAAGGCCCAAGGCGCTGTTTAAGCTGCC	1620
Db	1519	TCGCGGGCTTACCAAGGTGGCTGATGCGGTCAAGGCCCAAGGCGCTGTTTAAGCTGCC	1578
OY	1621	AGGCGCCAAAGCCACGGCTCACCGGGCAATCCAAACCAACTCMAACGCGCCAGAGACTTTT	1680
Db	1579	AGGCGCCAAAGCCACGGCTCACCGGGCAATCCAAACCAACTCMAACGCGCCAGAGACTTTT	1638
OY	1681	CGAAGCGGGCGCTTTTTCAGAGCCAGGGGCGCTCACTGCGCTTCAATAACCTGTACTTT	1740
Db	1639	CGAAGCGG--GCTTTTTCAGAGCCAGGGGCGCTCACTGCGCTTCAATAACCTGTACTTT	1698
OY	1741	GCGCGCGGTGCCCTGTGCATTTCCACCCCAAGAAAGATGACGCGCACTTGACTGTACAGGA	1800
Db	1697	GCGCGCGGT--CCCTGTGCATTTCCACCCCAAGAAAGATGACGCGCACTTGACTGTACAGGA	1754
OY	1801	CGGCACTTTTTCGCGAGCGGCGGTACCCCGAGAGGCTGTCCTCCCGAGGCGCTTAAGC	1860
Db	1755	CGGCACT--TTTTTCGCGAGCGGCGGTACCCCGAGAGGCTTCTTCCCGAGGCGCTTAAGC	1812
OY	1861	GCTGACGTGCGCCCGGACTTTTGTGCTTCGACATTCGCTCGGTTTTTGACCCCGCTCAAGTATCC	1920
Db	1813	GCTGACGT--GCCCGACTTTTGTGCTTCGACATTCGCTCGGTTTTTGACCCCGCTCAAGTATCC	1870
OY	1921	CACCTGTGTGTGAAGCTTACCAAGCTCAATTGCTTTTATGTATATGTGGCCCCCTCTCTGC	1980
Db	1871	CACCTGTGT--TGAAGCTTACCAAGCTCAATTGCTTTTATGTATATGTGGCCCCCTCTCTGC	1928

0Y	1981	CCCCGAATTTTCCCTCCCATAGAGAGTCGCGTCTCTTACCTCGGTGACCCCAAGTGCAGTT	2040
Db	1929	CCCCGAA--TTCCCTGCATGAGAGTCGCGTCTCTTACCTCGGTGACCCCAAGTGCAGTT	1986
0Y	2041	AGTGTGGTGCTGCTGCGCTGCGCTGCCGGGATCGATCTGTAGCTGAGAGTCTTGT	2100
Db	1987	AGTGTGC--GCTTGGCCCTGCGCTGCGCGGATCGATCTGTGACCTGAGAGTCTTGT	2044
0Y	2101	GTAAACACGACGAGTCATAAAAAAAAAAAAAAAAAAAAAA	2139
Db	2045	GTAAACACCGAGTCAAAAAAAAAAAAAAAAAAAAAA	2083
RESULT 13			
ADQ36723	ID	ADQ36723 standard; cDNA; 2084 BP.	
AC	ADQ36723;		
DT	23-SEP-2004	(first entry)	
DE	Full-length NADP-GDH cDNA clone, SEQ ID 18.		
KM	Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;		
XX	NADP-specific GDH; NADP-specific glutamate dehydrogenase; ss.		
OS	Chlorella sorokiniana.		
PN	US2004128710-A1.		
XX			
PD	01-JUL-2004.		
XX			
PF	24-JUL-2003; 2003US-00627886.		
PR	01-MAY-1998; 98US-00070844.		
PA	(SCHM/) SCHMIDT R R.		
PA	(MILL/) MILLER P.		
PI	Schmidt RR, Miller P;		
XX			
DR	WPI; 2004-533134/51.		
XX			
PT	Increasing or decreasing nitrogen metabolism in plant cells, for plant		
PT	with increased yield and improved tolerance to ammonia toxicity and		
PT	osmotic stress, by transforming plant cell with nucleic acid having		
PT	glutamate dehydrogenase activity.		
Example 2; SEQ ID NO 18; 36pp; English.			
XX			
CC	The present invention relates to increasing or decreasing the nitrogen		
CC	metabolism in plant cells by transforming a plant cell with a		
CC	polynucleotide encoding a polypeptide having glutamate dehydrogenase		
CC	(GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH		
CC	(ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,		
CC	ADQ36731), or their fragments, which exhibits GDH activity. The		
CC	polynucleotide is operably linked to a polynucleotide encoding a		
CC	chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their		
CC	fragments that exhibit chloroplast transit activity. The method is useful		
CC	for increasing or decreasing the nitrogen metabolism in plant cells. The		
CC	methods, polynucleotides, and polypeptides are useful in producing plant		
CC	with increased yield, and with improved tolerance to ammonia toxicity,		
CC	osmotic stress, and composition of the crop or plant. The present		
CC	sequence is a cDNA clone which was isolated during the isolation of the		
CC	NADP-specific GDH cDNAs of the invention. Ten NADP-GDH clones were		
CC	identified in an example from the invention. Sequence analysis revealed		
CC	all ten clones were identical at their 3' termini and differed by varying		
CC	degree of truncation at their 5' termini. Clone PBGDc53 (ADQ36712) was		
CC	the longest clone and was found to have a complete 3' terminus, but was		
CC	not long enough to encode either NADP-GDH subunit and so PCR was carried		
CC	out to determine the 5' terminal sequence using primers ADQ36713-ADQ36717		
CC	ADQ36720, resulting in isolation of the 5' cDNA clones PBGdc 60		
CC	(ADQ36718), PBGdc 61 (ADQ36719), PBGdc 63 (ADQ36721) and PBGdc 64		





Db 1990 GTGCTGCTTGGCCCTGCGCTGCCCGGAGTCGATCTGACCTGAGAGTCTTG-- 2047  
Qy 2104 AACACGACGAGTCAAAAAAAAAAAAAAAAAAAAA 2140  
Db 2048 AACGACGAGTCAAAAAAAAAAAAAAAAAAAAA 2084  
RESULT 14  
ADQ36724  
ID ADQ36724 standard; cDNA; 2045 BP.  
XX  
AC ADQ36724;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Full-length NADP-GDH cDNA clone, SEQ ID 19.  
XX  
KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;  
KW NADP-specific GDH; NADP-specific glutamate dehydrogenase; ss.  
XX  
OS Chlorella sorokiniana.  
XX  
PN US2004128710-A1.  
XX  
PD 01-JUL-2004.  
XX  
PF 24-JUL-2003; 2003US-00627886.  
XX  
PR 01-MAY-1998; 98US-00070844.  
XX  
PA (SCHM/) SCHMIDT R R.  
PA (MILL/) MILLER P.  
PI Schmidt RR, Miller P;  
PI  
XX WPI; 2004-533134/51.  
XX  
DR  
PT Increasing or decreasing nitrogen metabolism in plant cells, for plant  
PT with increased yield and improved tolerance to ammonia toxicity and  
PT osmotic stress, by transforming plant cell with nucleic acid having  
PT glutamate dehydrogenase activity.  
XX  
XX  
XX Example 2; SEQ ID NO 19; 36bp; English.  
XX  
PS The present invention relates to increasing or decreasing the nitrogen  
XX metabolism in plant cells by transforming a plant cell with a  
CC polynucleotide encoding a polypeptide having glutamate dehydrogenase  
CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,  
CC ADQ36731), or their fragments, which exhibits GDH activity. The  
CC polynucleotide is operably linked to a polynucleotide encoding a  
CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their  
CC fragments that exhibit chloroplast transit activity. The method is useful  
CC for increasing or decreasing the nitrogen metabolism in plant cells. The  
CC methods, polynucleotides, and polypeptides are useful in producing plant  
CC with increased yield, and with improved tolerance to ammonia toxicity,  
CC osmotic stress, and composition of the crop or plant. The present  
CC sequence is a cDNA clone which was isolated during the isolation of the  
CC NADP-specific GDH cDNAs of the invention. Ten NADP-GDH clones were  
CC identified in an example from the invention. Sequence analysis revealed  
CC all ten clones were identical at their 3' termini and differed by varying  
CC degree of truncation at their 5' termini. Clone pBGD53 (ADQ36712) was  
CC the longest clone and was found to have a complete 3' terminus, but was  
CC not long enough to encode either NADP-GDH subunit and so PCR was carried  
CC out to determine the 5' terminal sequence using primers ADQ36713-ADQ36717  
CC and ADQ36720, resulting in isolation of the 5' cDNA clones pBGD 60  
CC (ADQ36718), pBGD 61 (ADQ36719), pGD 63 (ADQ36721) and pGD 64  
CC (ADQ36722) and the full-length clones ADQ36723 and ADQ36724.  
XX  
SQ Sequence 2045 BP; 402 A; 697 C; 598 G; 348 T; 0 U; 0 Other;  
Query Match 75.3%; Score 1611; DB 12; Length 2045;  
Best Local Similarity 95.6%; Pred. No. 4.6e-257;

Matches 2044; Conservative 0; Mismatches 0; Indels 93; Gaps 34;  
Qy 4 CTTTCTGCTGCTCCCTCTCTCCGTCATGACGACCGCCCTGTCGCAAGCTATCG 63  
Db 1 CTTTCTGCTGCTCCCTCTCTCCGTCATGACGACCGCCCTGTCGCAAGCTATCG 60  
Qy 64 TGGCGCCCGCTGGCGGCAAGCCCGGCTGCTCCGCGCCGTGGCCGTGGGTCC 123  
Db 61 TGGCC-----TGCGCTGGGTCC 78  
Qy 124 GCTCCGCAAGCGGATGTCGCGGCCAAGGCGGTCCTGCTGGAAGACATCTCCGCA 183  
Db 79 GCTCCGCAAGCGGATGTCGCGGCCAAGGCGGTCCTGCTGGAAGACATCTCCGCA 137  
Qy 184 TGAAGCCCAACCAACCGGCGACTTCACGCGCTGAGAGAGCGGTGAAGACAGATGCGCA 243  
Db 138 TGAAGCCCAACCAACCGGCGACTTCACGCGCTGAGAGAGCGGTGAAGACAGATGCGCA 196  
Qy 244 AGCGGCGCACTGAGAGGCTGCTGTCACGCGATCAAGAAACCCGACGTGCGCAAGCTTCA 303  
Db 197 AGCGGCGCACTGAGAGGCTGCTGTCACGCGATCAAGAAACCCGACGTGCTGCA 255  
Qy 304 CCGAGATCTTCATGAAGAACCCGAGACGAGAGATTCAAGCGCGGTGCGGAGGTG 363  
Db 256 CCGAGATCTTCATGAAGAACCCGAGACGAGAGATTCAAGCGCGGTGCGGAGGTG 314  
Qy 364 CCGTCTCCCTGACGCGCCGCTGTCAGAGAGCGCCCGAGCTGCTGCCATCTTCAAGCAGA 423  
Db 315 CCGTCTCCCTGACGCGCCGCTGTCAGAGAGCGCCCGAGCTG-TGCCATCTTCAAGCAGA 373  
Qy 424 TCGTTAGCTGAGCGCGGTATCACTTCCGCGTGTCTGCTGAGACAGCGCGCAAC 483  
Db 374 TCGTTAGCTGAGCGCGGTATCACTTCCGCGTGTCTGCTG-TGACAGAGCGCGCAAC 432  
Qy 484 TGACGGTCAACCGGCGCTCCGCGTGCAGTACTGTCGCGCATCGCGCCCTCAAGAGGCG 543  
Db 433 TGACGGTCAACCGGCGCTCCGCGTGCAGTACTGTCGCGCATCGCGCCCTCAAGAGGCG 491  
Qy 544 GCTGCGCTTCAACCCCTCCGTCGAACCTGTCAATCAAGAGTTCCTTGAAGCAGA 603  
Db 492 GCTGCGCTTCAACCCCTCCGTCGAACCTGTCAATCAAGAG-TCTTGCTTTGAGCAGA 550  
Qy 604 TCTTCAAGAAACGCTTGAACACCTTCCCATGCGCGCGGCAAGGCGGCTCCGACTTCG 663  
Db 551 TCTTCAAGAAACGCTTGAACACCTTCCCATGCGCGCGGCAAGGCGGCTCCGACTTCG 609  
Qy 664 ACCCAAGGCGCAAGAGGAGCGGAGGTGATGCGCTTCTGCACTTCATGACGAGC 723  
Db 610 ACCCAAGGCGCAAGAGGAGCGGAGGTGATGCGCTTCTG-CACTTCATGACGAGC 668  
Qy 724 TGACGCGCACATCAAGCTAGCGAGAGCTGCGCGCGCGCAATCGCGGTGGCGCG 783  
Db 669 TGACGCGCACATCAAGCTAGCGAGAGCTGCGCGCGCGCAATCGCGGTGGCGCG 727  
Qy 784 GCGAGATGCTGCTATCTTTTGGCCAGTACAAAGGCGATCAACGAGCTGCGCTGC 843  
Db 728 GCGAGATGCTGCTATCTTTTGGCCAGTACAAAGGCGATCAACGAGCTGCGCTGC 786  
Qy 844 TGACCCGGAAGGCGCAGAGATATGCGCGCTCCGAGATCCGCCGAGGCGCAAGGCTTACG 903  
Db 787 TGACCCGGAAGGCGCAGAGATATGCGCGCTCCGAGATCCG-CGAGGCGCAAGGCTTACG 845  
Qy 904 GCGCGCTGCTGTTTGTGAGAAAGCTGTGAAGGCAAGGCGAGAGCTTCAAGGCGCAAGC 963  
Db 846 GCGCGCTGCTGTTTGTGAGAAAGCTGTGAAGGCAAGGCG-AGAGCTTCAAGGCGCAAGC 904  
Qy 964 GCTGCTGTGTGTGCGCGCGGCAAGTGGCCAGTACTGCGGAGAGCTGCTGTGAGA 1023  
Db 905 GCTGCTGTGTGTGCGCGCGGCAAGTGGCCAGTACTGCG-AGAGCTGCTGTGTGAGA 963  
Qy 1024 AGGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
Db 964 AGGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1021



Oy	1084	TCACGCGGAGAGCTGGACGGGGGGTGCAGACATGAAGAAGAAACAACGGCGCGCA	1143
Db	1022	TCACGCGGAGAGCTGCAGGGCGGTGCAGACATGAAGA--AAGAACAACAGCGCCGCCA	1078
Oy	1144	TCTCCGAGTACAAGAGCGACACCGCGGTGTATGTGGGCGACCGCGCAAGCTTGGAGC	1203
Db	1080	TCTCCGAGTACAAGAGCGACACCGCGGTGTATGTGGGCGA--GCCGAAGCTTGGAGC	1137
Oy	1204	TGGAATGCGAGGTGGAACAATCGCTTCCCTGGGCCACCCAGAAGAGATTCATGAGACG	1265
Db	1138	TGGAATGCGAGGTGGAACAATCGCTTCCCTGGGCCACCC--AAGAGATTCATGAGACG	1195
Oy	1264	ACGCGGAGCTCTGATTCAGACACGGCTGCAGTACGTGTGGAGGGGCCCAATGACCT	1323
Db	1196	ACGCGGAGCTCTGATTCAGACACGGCTGCAGTACGTGT--AGGCGCCAAATGCTCT	1255
Oy	1324	CCACCAACGAGGCGCATCCACAAGTACAAGGCGCGCATCTACTTGCCTCCGCAAGG	1383
Db	1254	CCACCAACGAGGCGCATCCACAAGTACAAGGCGCGCAT--TCTACTGCCCCGCAAGG	1311
Oy	1384	CGGCGCAACGCGGGCGGTGGCGGTACAGCGGCTGGAAGATGACCCAGAACCGGATGAGCC	1443
Db	1312	CGGCGCAACGCGGGCGGTGGCGGTACAGCGGCTTGAAGAT--CCAGAACCGGATGAGCC	1368
Oy	1444	TGAATCTGACTCGCGAGAGAGTTTCGCGACAAGCTGGAAGCGCATCTGAGACATCTACG	1503
Db	1370	TGAATCTGACTCGCGAGAGAGTTTCGCGACAAGCTGAGAGC--TCAATGAAGGACATCTACG	1427
Oy	1504	ACTCCGCGCATGGGGCGCTTCCGCGAGTACAATGTGTACTGTGCTTCCGGCGCCCAACATCG	1566
Db	1428	ACTCCGCGCATGGGGCGCTTCCGCGAGTACAATGTGTACT--TTCGCGGCGCGCAACATCG	1485
Oy	1564	CGGCGTTTACCAAGAGTGGCTGATGTCGTCAAGGCCAGGCGGCTGTTAAGCTGGCCAGG	1623
Db	1486	CGGCGTTTACCAAGAGTGGCTGATGTCGTTCMAAGGCCAGG--GCTGTTAAGCTGGCCAGG	1543
Oy	1624	CCCAAGCCACGAGCTTCAACCGGCGAATCCCAACCAACTCAACGCGCAAGACCTTTTCGG	1683
Db	1544	CCCAAGCCACGAGCTTCAACCGGCGAATCCCAACCAACTC--CGGCGAGGACCTTTTCGG	1601
Oy	1684	AAGGCGGCGCTTTTCCAGCGAGGGGCCCTACCTGCGCCCTTTCATACCTCGTATTTGCC	1743
Db	1602	AAGGCGGCGCTTTTCCAGCGAGGGGCCCTACCTGCGCC--TCATPACCTTGTATTTGCC	1655
Oy	1744	GCGGTGCCCTGCAATTCACCCCAAGAAGACTAGCGGCACTTGACTGCAATCAGACGG	1803
Db	1660	GCGGTGCCCTGCAATTCACCCCAAGAAGACTAGCGG--CTTGACTGCAATCAGACGG	1717
Oy	1804	CTATTTTTTTTGGCGACGGCGCTCACCCCGAGAGCCTCTCTCCCTCGAGCCTTAAGCCT	1863
Db	1718	CTATTTTTTTTGGCGACGGCGCTCACCCCGAGAGC--CTCTCCCTCGAGCCTTAAGCCT	1775
Oy	1864	GACGTCGCGCCGCACTTTGCTCGACATCGCTCGGTTTTGAACCCCTCGAGCTTACCGAC	1922
Db	1776	GACGTCGCGCCGCACTTTGCTCGACATCGCTCGGTTTTG--CCCTCGAGCTTACCGAC	1833
Oy	1924	CTGTGTGTGAAGCCTACAGGCTCAATTGCTTTTATGTATGTGGCCCGCTCTGCGCC	1983
Db	1834	CTGTGTGTGAAGCCTACAGGCTCAATTGCTTTTATGTAT--TGGCGCCCGCTCTGCGCC	1891
Oy	1984	GGAATTTTCTCGCCATGAGAGGTGGGTTCCTAGCGTGTGACCCCAAGTATGAGCTTGT	2043
Db	1892	GGAATTTTCTCGCCATGAGAGGTGGGTTCCTAGCGTGT--CCCAAGTATGAGCTTGT	1949
Oy	2044	GTCGTCGCTTTCCTCGCGCTGCGCCCGGAGATGCGATCTGTGACCTGAGAGTCTTGTGTA	2103
Db	1950	GTCGTCGCTTTCCTCGCGCTGCGCCCGGAGATGCGATCTGT--CTGAGAGTCTTGTGTA	2007
Oy	2104	AAACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140	
Db	2008	AAACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2044	

RESULT 15  
 AD036712  
 ID AD036712 standard; cDNA, 1922 BP.  
 XX  
 AC AD036712;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE NADP-specific GDH related clone pBGDC53, SEQ ID 7.  
 XX  
 KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;  
 XX NADP-specific GDH; NADP-specific glutamate dehydrogenase; ss.  
 OS  
 Chlorrella sorokiniana.  
 XX  
 PN US2004128710-A1.  
 PD  
 01-JUL-2004.  
 XX  
 PF 24-JUL-2003; 2003US-00627886.  
 XX  
 PR 01-MAY-1998; 98US-00070844.  
 XX  
 PA (SCHMIDT R R.  
 XX (MILLER P.  
 XX  
 PI Schmidt RR, Miller P;  
 XX  
 DR WPI, 2004-533134/51.  
 XX  
 PT Increasing or decreasing nitrogen metabolism in plant cells, for plant  
 PT with increased yield and improved tolerance to ammonia toxicity and  
 PT osmotic stress, by transforming plant cell with nucleic acid having  
 PT glutamate dehydrogenase activity.  
 XX  
 PS Example 2; SEQ ID NO 7; 36pp; English.  
 XX  
 CC The present invention relates to increasing or decreasing the nitrogen  
 CC metabolism in plant cells by transforming a plant cell with a  
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase  
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
 CC (AD036710), or their fragments, which exhibits GDH activity. The  
 CC AD036711, AD036729), a beta subunit of NADP-specific GDH (AD036709,  
 CC polynucleotide is operably linked to a polynucleotide encoding a  
 CC chloroplast transit peptide comprising AD036710 or AD036711, or their  
 CC fragments that exhibit chloroplast transit activity. The method is useful  
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The  
 CC methods, polynucleotides, and polypeptides are useful in producing plant  
 CC with increased yield, and with improved tolerance to ammonia toxicity,  
 CC osmotic stress, and composition of the crop or plant. The present  
 CC sequence is a cDNA clone which was isolated during the isolation of the  
 CC NADP-specific cDNA clones of the invention. Ten NADP-GDH clones were  
 CC identified in an example from the invention. Sequence analysis revealed  
 CC all ten clones were identical at their 3' termini and differed by varying  
 CC degree of truncation at their 5' termini. Clone pBGDC53 (AD036712) was  
 CC the longest clone and was found to have a complete 3' terminus, but was  
 CC not long enough to encode either NADP-GDH subunit and so PCR was carried  
 CC out to determine the 5' terminal sequence using primers AD036713-AD036717  
 CC and AD036720, resulting in isolation of the 5' cDNA clones pBGDC 60  
 CC (AD036718), pBGDC 61 (AD036719), pBGDC 63 (AD036721) and pBGDC 64  
 CC (AD036722) and the full-length clones AD036723 and AD036724.  
 XX  
 SQ Sequence 1922 BP, 393 A; 638 C; 567 G; 324 T; 0 U; 0 Other;  
 Query Match 73.1%; Score 1565; DB 12; Length 1922;  
 Best Local Similarity 97.6%; Pred. No. 1.8e-249;  
 Matches 1922; Conservative 0; Mismatches 0; Indels 47; Gaps 31

Qy 231 CAGATGGCCACCAAGGCGGCACTGAGGGCCCTGGTGCACGCGCATCAAGAACCCCGACGTG 290  
Db 61 CAGATGGCCACCAAGGCGGCACTGAGGGCCCTGGTGCACGCGCATCAAGAACCCCGACGT- 119  
Qy 291 CGCCAGCTGCTGACCCGAGATTTTCAATGAAGACCCGAGACAGCAGAGTTTATGAGGCG 350  
Db 120 CGCCAGCTGCTGACCCGAGATTTTCAATGAAGACCCGAGACAGCAGAGTTTATGAGGCG- 178  
Qy 351 GTGGCGGAGGTGGCGGTCTCCCTGACGCGGTGTTTCGAGAGCGCCCGAGCTGCTGCGC 410  
Db 179 GTGGCGGAGGTGGCGGTCTCCCTGACGCGGTGTTTCGAGAGCGCCCGAGCTGCTG-CC 237  
Qy 411 ATCTTCAAGCAGATGTTGAGCCTGAGCGCGTGAATCACTTCCGCGTGTCTGTGCTGAGC 470  
Db 238 ATCTTCAAGCAGATGTTGAGCCTGAGCGCGTGAATCACTTCCGCGTGTCTGTGCTGAG- 296  
Qy 471 GAGCGCGGCAACTGACAGTCAACCGCGGCTTCCGCGTGCAGTACTGCTCCGCCATCGGC 530  
Db 297 GAGCGCGGCAACTGACAGTCAACCGCGGCTTCCGCGTGCAGTACTGCTCCGCCATCGG- 355  
Qy 531 CCCTTCAAGGCGGCGGCTGCGCTTCCACCCCTCCGTTGAACCTGTGCATGATGAAGTTCTT 590  
Db 356 CCCTTCAAGGCGGCGGCTGCGCTTCCACCCCTCCGTTGAACCTGTGCATGATGAAGTTCT- 414  
Qy 591 GCCTTTGAGCAGATCTTCAAGACAGCCTGACCACTGCGCCATGAGGCGGCGCAAGGCG 650  
Db 415 GCCTTTGAGCAGATCTTCAAGACAGCCTGACCACTGCGCCATGAGGCGGCGGCAAGG- 473  
Qy 651 GGCCTCCGACTTTCGACCCCAAGGCGAAGAGCGACCGGAGGTGATGCGCTTCTGCCAGTCC 710  
Db 474 GGCCTCCGACTTTCGACCCCAAGGCGAAGAGCGACCGGAGGTGATGCGCTTCTGCCAGT- 532  
Qy 711 TTCAATGACCGGAGCTGACGCGCAATCATGAGTGAAGAGCGGCGCGCGGAGACATC 770  
Db 533 TTCAATGACCGGAGCTGACGCGCAATCATGAGTGAAGAGCGGCGCGGAGACAT- 591  
Qy 771 GGCCTGAGCGCGCGCGAGATTGAGTACCTTTTTCGCGCAGTACCAAGCGCATCCCAAGAC 830  
Db 592 GGCCTGAGCGCGCGCGAGATTGAGTACCTTTTTCGCGCAGTACCAAGCGCATCCCAAG- 650  
Qy 831 TACACCGGCGGTGACCCCGAAGGCGCAAGATGAGCGGCTCCGAGATCCGCCGAG 890  
Db 651 TACACCGGCGGTGACCCCGAAGGCGCAAGATGAGCGGCTCCGAGATCCGCCGAG- 709  
Qy 891 GCCACCGGCTAGCGGCGCGGTGCTGTTTGTGAGAACGCTGAAAGGACCAAGGCGAGAGC 950  
Db 710 GCCACCGGCTAGCGGCGCGGTGCTGTTTGTGAGAACGCTGAAAGGACCAAGGCGAG- 768  
Qy 951 CTCAAGGCGCAAGCGCTGCTGATGCTGCGCGGCAAGTGTGCGCCAGTACTGCGCGAG 1010  
Db 769 CTCAAGGCGCAAGCGCTGCTGATGCTGCGCGGCAAGTGTGCGCCAGTACTGCGCGAG- 827  
Qy 1011 CTGCTGCTGAGAGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070  
Db 828 CTGCTGCTGAGAGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG- 886  
Qy 1071 GAGCGCCAAACGCTTACGCGCGGAGACAGTGAAGCGGCTGAGCAATGAAGAAAGAAC 1130  
Db 887 GAGCGCCAAACGCTTACGCGCGGAGACAGTGAAGCGGCTGAGCAATGAAGAAAGAAC- 945  
Qy 1131 AACAGCGCGCGCATCTCCGATGATCAAGAGCAGACCGCGCTGTATGTGTGAGCAGCGCGC 1190  
Db 946 AACAGCGCGCGCATCTCCGATGATCAAGAGCAGACCGCGCTGTATGTGTGAGCAGCG- 1003  
Qy 1191 AAGCTTTGGAGCTGAGCTGCAAGTGAATCGCTTTCCCTGCGCCACCCAGAACGAG 1250  
Db 1004 AAGCTTTGGAGCTGAGCTGCAAGTGAATCGCTTTCCCTGCGCCACCCAGAAC--G 1061  
Qy 1251 ATGATATGAGCAGAGCGCGAGCTGCTGATCAAGAGCAGCGCTGCCAGTACGTGTGAGAGGC 1310  
Db 1062 ATGATATGAGCAGAGCGCGAGCTGCTGATCAAGAGCAGCGCTGCCAGTACGTGTGAGAG- 1119  
Qy 1311 GCCAATGATGCTCTCACCACCAAGAGGCGCATCCACAAGTACCAAGAGCGCGCATCATCTAC 1370

Db 1120 GCCAATGATGCTCTCACCACCAAGAGGCGCATCCACAAGTACCAAGAGCGCGCATCATCT- 1177  
Qy 1371 TGCCCCCGGCAAGGCGGCAAGCGCGGCGGTGCGCGGTTCAGCGGCTTGGAGATGACCCAG 1430  
Db 1178 TGCCCCCGGCAAGGCGGCAAGCGCGGCGGTGCGCGGTTCAGCGGCTTGGAGATGACCC- 1235  
Qy 1431 AACGCATGAGCCTGAATGAGTCTGCGAGAGAGTTCGCAACAAGCTGAGCGCATCATG 1490  
Db 1236 AACGCATGAGCCTGAATGAGTCTGCGAGAGAGTTCGCAACAAGCTGAGCGCATCA- 1293  
Qy 1491 AAGGACATCTAAGCATCCGCGCATGAGGCGGTCCCGCAGATGACATGTTGACTGCG 1550  
Db 1294 AAGGACATCTAAGCATCCGCGCATGAGGCGGTCCCGCAGATGACATGTTGACTGCGCT- 1351  
Qy 1551 GGCAGCAATCTGCGGCGCTTCAACAGTGTGATATCCCTCAAGGCGCCAGGCGCTGTT 1610  
Db 1352 GGCAGCAATCTGCGGCGCTTCAACAGTGTGATATCCCTCAAGGCGCCAGGCGCTG- 1409  
Qy 1611 TAACTGCGCGAGGCGCAAGCGCATCGGCTCAACGCGCATCCAACTCAACGCGCC 1670  
Db 1410 TAACTGCGCGAGGCGCAAGCGCATCGGCTCAACGCGCATCCAACTCAACGCG- 1467  
Qy 1671 AAGACCTTTTTCGAGAGCGGCGCTTTTTCGAGCAGAGGCGCTTCACTGCGCTTTCATTA 1730  
Db 1468 AAGACCTTTTTCGAGAGCGGCGCTTTTTCGAGCAGAGGCGCTTCACTGCGCTTTCAT- 1525  
Qy 1731 CCTGCTATTTGCGCGCGCTGCGCTGCAATTCACCCCAAGAAACAAAGGAGGAGCTTGAC 1790  
Db 1526 CCTGCTATTTGCGCGCGCTGCGCTGCAATTCACCCCAAGAAACAAAGGAGGAGCTTG- 1583  
Qy 1791 TGATCAGAGACGCGTATTTTTCGAGCAGCGCGCTCAACCCGAGAGAGCTCTCTCCCGC 1850  
Db 1584 TGATCAGAGACGCGTATTTTTCGAGCAGCGCGCTCAACCCGAGAGAGCTCTCTCCCG- 1641  
Qy 1851 AGCCCTTAAAGCGCTGACGCTGCGCGCGCATTTTGTGCTGCAATGCTGCGTTTGAACCCCT 1910  
Db 1642 AGCCCTTAAAGCGCTGACGCTGCGCGCGCATTTTGTGCTGCAATGCTGCGTTTGAACCC- 1699  
Qy 1911 CCACTTACCAACCCCTGTTGAGAGCCTTACAGCTGAATTGCTTTAGTGTATGTGCGC 1970  
Db 1700 CCACTTACCAACCCCTGTTGAGAGCCTTACAGCTGAATTGCTTTAGTGTATGT- 1757  
Qy 1971 CCCCTCTGCGCGCGAATTTTCTGCGCATGAGAGCTGCGGTTCTTACCTGAGTACCCCA 2030  
Db 2031 AGTAGAGTTAGTGTGCGGCTGCTGCGCTGCGCTGCGCGGATGCGATTACTGTGACCTGA 2090  
Qy 1816 AGTAGAGTTAGTGTGCGGCTGCTGCGCTGCGCTGCGCGGATGCGATTACTGTGACCT- 1873  
Db 2091 GAGTGTGTTGTATAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2139  
Qy 1874 GAGTGTGTTGTATAACACGAGTCAAAAAAAAAAAAAAAAAAAAAA 1922

Search completed: July 9, 2005, 19:27:18  
Job time : 1088 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2005, 18:17:32 ; Search time 379 Seconds

(without alignments)  
9239.135 Million cell updates/sec

Title: US-10-627-886-1  
Perfect score: 2140  
Sequence: 1 CTCCTTCTGCTGCCCTCT.....AAAAAAAAAAAAAAAAAAAA 2140

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PTCTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2140	100.0	2140	2	US-08-541-033A-1
2	2140	100.0	2140	2	US-08-828-451-1
3	2137	99.9	2137	2	US-08-541-033A-18
4	2137	99.9	2137	2	US-08-828-451-18
5	2046	95.6	2099	2	US-08-541-033A-3
6	2046	95.6	2099	2	US-08-828-451-3
7	2043	95.5	2096	2	US-08-541-033A-19
8	2043	95.5	2096	2	US-08-828-451-19
9	1969	92.0	1969	2	US-08-541-033A-7
10	1969	92.0	1969	2	US-08-828-451-7
11	1501.4	70.2	1506	2	US-08-541-033A-23
12	1501.4	70.2	1506	2	US-08-828-451-23
13	1470	68.7	1473	2	US-08-541-033A-25
14	1470	68.7	1473	2	US-08-828-451-25
15	592.2	27.7	1497	4	US-09-252-991A-4131
16	590.8	27.6	1353	4	US-09-252-991A-4075
17	451.6	21.1	1359	4	US-09-489-039A-766
18	435.6	20.4	1359	4	US-08-508-761B-5
19	393.8	18.4	1937	1	US-08-370-193A-10
20	392.2	18.3	1482	2	US-08-886-640-5
21	392.2	18.3	1482	3	US-08-884-235-13
22	392.2	18.3	1489	2	US-08-886-640-4
23	392.2	18.3	1489	3	US-08-884-235-12
24	392.2	18.3	1501	2	US-08-886-640-6
25	392.2	18.3	1501	3	US-08-884-235-14
26	392.2	18.3	1659	2	US-08-886-640-1
27	392.2	18.3	1659	2	US-08-886-640-2

28	392.2	18.3	1659	3	US-08-884-235-1	Sequence 1, Appli
29	392.2	18.3	1659	3	US-08-884-235-2	Sequence 2, Appli
30	341	15.9	1266	3	US-08-961-697-137	Sequence 137, App
31	338.6	15.8	2816	3	US-09-171-337A-1	Sequence 1, Appli
32	338.6	15.8	2816	3	US-09-631-022-1	Sequence 1828, Ap
33	334.8	15.6	1347	4	US-09-583-110-1828	Sequence 4059, Ap
34	315.6	14.7	1221	4	US-09-252-991A-4059	Sequence 13, Appl
35	311	14.5	367	2	US-08-541-033A-13	Sequence 13, Appl
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37	308	14.4	308	2	US-08-541-033A-16	Sequence 16, Appl
38	308	14.4	308	2	US-08-828-451-16	Sequence 16, Appl
39	303	14.2	39003	4	US-09-596-002-21	Sequence 2485, Ap
40	286.2	13.4	1341	4	US-09-543-681A-2485	Sequence 1438, Ap
41	284.8	13.3	1106	4	US-09-107-433-1438	Sequence 1599, Ap
42	265.2	12.4	1404	4	US-09-328-352-1599	Sequence 479, App
43	261	12.2	1347	4	US-09-134-000C-479	Sequence 4053, Ap
44	251	11.7	1530	4	US-09-902-540-4053	Sequence 1201, Ap
45	251	11.7	21511	4	US-09-902-540-1201	

#### ALIGNMENTS

RESULT 1  
US-08-541-033A-1  
Sequence 1, Application US/08541033A

Patent No. 5879941

GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESSES:

ADDRESS: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/541,033A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Whitlock, Ted W.

REGISTRATION NUMBER: 36,965

REFERENCE/DOCKET NUMBER: UP155

TELECOMMUNICATION INFORMATION:

TELEPHONE: (904) 375-8100

TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2140 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 33...1610

US-08-541-033A-1

Query Match 100.0%; Score 2140; DB 2; Length 2140;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2140; Conservative 0; Mismatches 0; Indels 0;

QY 1 CTCCTTCTGCTCGCCCTCTCTCGCTCCGCGCATGACAGCCGCGCTGTCGCAAGCTA 60  
Db 1 CTCCTTCTGCTCGCCCTCTCTCGCTCCGCGCATGACAGCCGCGCTGTCGCAAGCTA 60  
QY 61 TCGTGGCCGCGCCGCTGCGCGCACGCGCGCTGCTTGGCGCGCTGGCCGCTGGG 120  
Db 61 TCGTGGCCGCGCCGCTGCGCGCACGCGCGCTGCTTGGCGCGCTGGCCGCTGGG 120  
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Db 301 TGACCGAGATCTTATGAGAGACCCGAGCGAGCGAGTTGATGACAGCGGTGGCGAGG 360  
QY 361 TGGCGGTCTCCCTGACGCGCGTGTTCGAGAACGCGCGGAGCTGCGCATCTTCAAGC 420  
Db 361 TGGCGGTCTCCCTGACGCGCGTGTTCGAGAACGCGCGGAGCTGCGCATCTTCAAGC 420  
QY 421 AGATGTTGAGCTGAGCGCGGTATCACCTTCCGCGTGTCTGTGCTGAGACGCGCA 480  
Db 421 AGATGTTGAGCTGAGCGCGGTATCACCTTCCGCGTGTCTGTGCTGAGACGCGCA 480  
QY 481 ACCTGCAAGTAAACGCGGCTTCCGCGTGCAGTACTGTCCGCGCATGGCGCCCTCAAGG 540  
Db 481 ACCTGCAAGTAAACGCGGCTTCCGCGTGCAGTACTGTCCGCGCATGGCGCCCTCAAGG 540  
QY 541 GCGGCTGCGCTTCCACCCCTCGGTGAACCTGTCAATCATGAATCTTTCCTTGGC 600  
Db 541 GCGGCTGCGCTTCCACCCCTCGGTGAACCTGTCAATCATGAATCTTTCCTTGGC 600  
QY 601 AGATCTTCAAGAACGCTGACACCTTGGCCATGGCGGCGCAAGGCGGCTCCGACT 660  
Db 601 AGATCTTCAAGAACGCTGACACCTTGGCCATGGCGGCGCAAGGCGGCTCCGACT 660  
QY 661 TCGACCCCAAGGGGCAAGGCGAGCGAGGTGATGCGCTTCTGCAAGTCTTCAATGACG 720  
Db 661 TCGACCCCAAGGGGCAAGGCGAGCGAGGTGATGCGCTTCTGCAAGTCTTCAATGACG 720  
QY 721 AGCTGACGCGCACATCACTACGTGACGAGACGTGCCCGCGGCAATCGGCGTGGCG 780  
Db 721 AGCTGACGCGCACATCACTACGTGACGAGACGTGCCCGCGGCAATCGGCGTGGCG 780  
QY 781 CGCGCGAGATTGGCTACTTTTTCGCGCAGTACAAAGCGCATCAAGAACTTCAACCGGCG 840  
Db 781 CGCGCGAGATTGGCTACTTTTTCGCGCAGTACAAAGCGCATCAAGAACTTCAACCGGCG 840  
QY 841 TCGTGAACCCCGAAGGGCCAGAGATGCGCGGCTCCGAGATCGCGCCGAGGCGACCGGCT 900  
Db 841 TCGTGAACCCCGAAGGGCCAGAGATGCGCGGCTCCGAGATCGCGCCGAGGCGACCGGCT 900  
QY 901 ACGGCGCGGCTGTGTTGTGAGAACTGTCTGAAGGACAAAGGCGAGAGCTTCAAGGCA 960  
Db 901 ACGGCGCGGCTGTGTTGTGAGAACTGTCTGAAGGACAAAGGCGAGAGCTTCAAGGCA 960  
QY 961 AGCGCTGCTGTGTCTGTGCGCGGCAAGTGGCCCACTGCGCGGAGCTGTGCTGG 1020  
Db 961 AGCGCTGCTGTGTCTGTGCGCGGCAAGTGGCCCACTGCGCGGAGCTGTGCTGG 1020  
QY 1021 AGAAGGGGCGCATGCTGTGTGCTGTCCGACTCCGAGGGCTTACGTGTGACAGGCCAAG 1080  
Db 1021 AGAAGGGGCGCATGCTGTGTGCTGTCCGACTCCGAGGGCTTACGTGTGACAGGCCAAG 1080  
QY 1081 GCTTCAAGCGCGAGAGCTGAGGCGGTGACAGCATGAAGAAAGAACAGCGGCC 1140

Db 1081 GCTTCAAGCGCGAGAGCTGAGGCGGTGACAGCATGAAGAAAGAACAGCGGCC 1140  
QY 1141 GCATCTCCAGATCAAGAGGACACCGCGCTGTATGTGGGCGACCGCGCAACCTTGGG 1200  
Db 1141 GCATCTCCAGATCAAGAGGACACCGCGCTGTATGTGGGCGACCGCGCAACCTTGGG 1200  
QY 1201 AGCTGACGCGCAGGTGACATGCGCTTCCCTGCGCGCACCCGAAAGCAGATGATGAGC 1260  
Db 1201 AGCTGACGCGCAGGTGACATGCGCTTCCCTGCGCGCACCCGAAAGCAGATGATGAGC 1260  
QY 1261 ACGACGCGGAGCTGTGATCAAGCAAGGCTGCCAGTACGTGTGAGAGGCGCAATGC 1320  
Db 1261 ACGACGCGGAGCTGTGATCAAGCAAGGCTGCCAGTACGTGTGAGAGGCGCAATGC 1320  
QY 1321 CTTTCAACCAAGAGGCGCATCAAGTACAAAGAGCGCGCATCATTTATGCCCCGGCA 1380  
Db 1321 CTTTCAACCAAGAGGCGCATCAAGTACAAAGAGCGCGCATCATTTATGCCCCGGCA 1380  
QY 1381 AGGCGGCGCAAGCGCGGCGGTGCGCGGCTGAGAGATGACCCAGAACCGCATGA 1440  
Db 1381 AGGCGGCGCAAGCGCGGCGGTGCGCGGCTGAGAGATGACCCAGAACCGCATGA 1440  
QY 1441 GCTGAACTGGAATCGCGAGAGGTTGCGCAAGCTGAGCGCATCATGAAGACATCT 1500  
Db 1441 GCTGAACTGGAATCGCGAGAGGTTGCGCAAGCTGAGCGCATCATGAAGACATCT 1500  
QY 1501 ACGACTCCGCGCATGAGGCGCTCCCGAGATACAAATGTTGACTGTGCGGCGGCGCAACA 1560  
Db 1501 ACGACTCCGCGCATGAGGCGCTCCCGAGATACAAATGTTGACTGTGCGGCGGCGCAACA 1560  
QY 1561 TCGGCGGCTTCAACCAAGTGGTGTATGCGCTCAAGGCGCGAGGCGCTGTTAAGCTGCC 1620  
Db 1561 TCGGCGGCTTCAACCAAGTGGTGTATGCGCTCAAGGCGCGAGGCGCTGTTAAGCTGCC 1620  
QY 1621 AGGCGCAAGCGACGCGCTCACCGCAATCAACCAACCAACTCAAGCGGCGAGACCTTTT 1680  
Db 1621 AGGCGCAAGCGACGCGCTCACCGCAATCAACCAACCAACTCAAGCGGCGAGACCTTTT 1680  
QY 1681 CGGAAAGGGGCGCTTTTTCGACGAGGCGCTCACCTGCGCTTTCATTAACCTGCTATT 1740  
Db 1681 CGGAAAGGGGCGCTTTTTCGACGAGGCGCTCACCTGCGCTTTCATTAACCTGCTATT 1740  
QY 1741 GCGCGGCGCTGCGCAATCAACCCCAAGAAAGCTGAGGCGCACTTGACTGACAGGA 1800  
Db 1741 GCGCGGCGCTGCGCAATCAACCCCAAGAAAGCTGAGGCGCACTTGACTGACAGGA 1800  
QY 1801 CGGCTATTTTTCGCGACGCGGCTTCAACCCGAGAGCTTCTTCCCGGAGCCTTAAGC 1860  
Db 1801 CGGCTATTTTTCGCGACGCGGCTTCAACCCGAGAGCTTCTTCCCGGAGCCTTAAGC 1860  
QY 1861 GCTGACGCTCGCGCGACTTTTTCGCGACATCGCTCGGTTTGAACCCCTCCAGTCAAC 1920  
Db 1861 GCTGACGCTCGCGCGACTTTTTCGCGACATCGCTCGGTTTGAACCCCTCCAGTCAAC 1920  
QY 1921 CACCGTGTGAGAGCTTACAGCTCAATGCTTTTATGTAATGTCGCGCCCTCTGCG 1980  
Db 1921 CACCGTGTGAGAGCTTACAGCTCAATGCTTTTATGTAATGTCGCGCCCTCTGCG 1980  
QY 1981 CCCGGAATTTTCTGCGCATGAGAGTGGGTTCTAGCTGTGACCCCAAGTACAGTT 2040  
Db 1981 CCCGGAATTTTCTGCGCATGAGAGTGGGTTCTAGCTGTGACCCCAAGTACAGTT 2040  
QY 2041 AGTGTGTCGCTTGGCGCTGCGCTGCGCGGAGATACATGTGACCTGAGAGTCTGT 2100  
Db 2041 AGTGTGTCGCTTGGCGCTGCGCTGCGCGGAGATACATGTGACCTGAGAGTCTGT 2100  
QY 2101 GTAAACAGCAGAGAGTCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 2140  
Db 2101 GTAAACAGCAGAGAGTCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 2140

RESULT 2

US-08-828-451-1  
Sequence 1, Application US/08828451  
Patent No. 5985634  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,451  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2140 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 33..1610  
US-08-828-451-1

Query Match 100.0%; Score 2140; DB 2; Length 2140;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTTCTGCTCCCTCTCTCTCCGTCGCCATGACAGCCGCTCGTCCCAAGCTTA 60  
DB 1 CTCCTTTCTGCTCCCTCTCTCTCCGTCGCCATGACAGCCGCTCGTCCCAAGCTTA 60  
QY 61 TCGTGGCCGCCCGCTGCGGCAAGCCCGCGCTGCGCGCTGCGCGCTGCGCGTGG 120  
DB 61 TCGTGGCCGCCCGCTGCGGCAAGCCCGCGCTGCGCGCTGCGCGCTGCGCGTGG 120  
QY 121 TCGGCTCGGCAAGCGGATGTCGCGCGCAAGGCGCTGCTGGAAGAGAGATCTCCG 180  
DB 121 TCGGCTCGGCAAGCGGATGTCGCGCGCAAGGCGCTGCTGGAAGAGAGATCTCCG 180  
QY 181 CGATGAGCGCCACCGCGCACTTTCAGCGGCTGCGAGAAAGCGGTGAAGAGATGCGCA 240  
DB 181 CGATGAGCGCCACCGCGCACTTTCAGCGGCTGCGAGAAAGCGGTGAAGAGATGCGCA 240  
QY 241 CCAAGGCGGGGCACTGAGGGCTGTGTGCAAGGCAATCAAGAACCCGAGCGTGGCGAGCTGC 300  
DB 241 CCAAGGCGGGGCACTGAGGGCTGTGTGCAAGGCAATCAAGAACCCGAGCGTGGCGAGCTGC 300  
QY 301 TGACGAGATCTTATGAAGACCGGAGACGAGAGATTATGACAGCGGTGCGCGAGG 360

DB 301 TGACGAGATCTTATGAAGACCGGAGACGAGAGATTATGACAGCGGTGCGCGAGG 360  
QY 361 TGGCGGTCTCCCTGACCGCGGTGTTGGAAGACCCCGAGCTGCTCCATCTTCAAGC 420  
DB 361 TGGCGGTCTCCCTGACCGCGGTGTTGGAAGACCCCGAGCTGCTCCATCTTCAAGC 420  
QY 421 AGATGTTGAGCGTGAAGCGGTGATGACCTTCCGCGTGTCTGCTGGAAGAGCGCGCA 480  
DB 421 AGATGTTGAGCGTGAAGCGGTGATGACCTTCCGCGTGTCTGCTGGAAGAGCGCGCA 480  
QY 481 ACTGCAAGTCAACCGCGGCTGCGGCTGCAAGTACTGTCGCGCATGAGCGCCCTCAAGG 540  
DB 481 ACTGCAAGTCAACCGCGGCTGCGGCTGCAAGTACTGTCGCGCATGAGCGCCCTCAAGG 540  
QY 541 GCGGCTGCGCTTCCACCCCTCCGTGAACCTGTCAATGAAAGTTCTTGCCTTTGAGC 600  
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DB 661 TCGACCCCAAGGCGCAAGCGACGCGGAGTATGCGCTTCTGCAAGTCTTCAAGC 720  
QY 721 AGCTGACGCGCCACATAGCTACGTGAGAGACGTGCGCGCGCGGACATGCGCGTGG 780  
DB 721 AGCTGACGCGCCACATAGCTACGTGAGAGACGTGCGCGCGCGGACATGCGCGTGG 780  
QY 781 CGGCGGAGATTGCTTACTTTTGGCCAGTACCAAGCCCATCAAGAACTACACCGGCG 840  
DB 781 CGGCGGAGATTGCTTACTTTTGGCCAGTACCAAGCCCATCAAGAACTACACCGGCG 840  
QY 841 TGCTGACCCGGAAGGCGCAGAGATGAGCGGCTCCAGATCCGCGCGGACCAAGCGCT 900  
DB 841 TGCTGACCCGGAAGGCGCAGAGATGAGCGGCTCCAGATCCGCGCGGACCAAGCGCT 900  
QY 901 ACGGCGCGGTGCTGTTTGTGAGAACGTGTGAAGAACAGGCGAGAGCTCAAGGCGCA 960  
DB 901 ACGGCGCGGTGCTGTTTGTGAGAACGTGTGAAGAACAGGCGAGAGCTCAAGGCGCA 960  
QY 961 AGCGCTGCTGTGTGTGCGGCGGCAAGTGGCCGAGTACTGCGCGAGACTGTGCTGG 1020  
DB 961 AGCGCTGCTGTGTGTGCGGCGGCAAGTGGCCGAGTACTGCGCGAGACTGTGCTGG 1020  
QY 1021 AGAAGGCGCGCATGAGCTGTCGCTGCGAGTCCCGAGGCTACGTTACGAGCCCAAG 1080  
DB 1021 AGAAGGCGCGCATGAGCTGTCGCTGCGAGTCCCGAGGCTACGTTACGAGCCCAAG 1080  
QY 1081 GCTTCAAGCGCGCAGCAGCTGCAAGCGGTGAGAGCATGAAAGAAAGAACAGCGCCC 1140  
DB 1081 GCTTCAAGCGCGCAGCAGCTGCAAGCGGTGAGAGCATGAAAGAAAGAACAGCGCCC 1140  
QY 1141 GCATCTTCAAGTACAAAGAGGACACCGCGCTGTATGTGTGGCGACCGCGCAAGCTTGG 1200  
DB 1141 GCATCTTCAAGTACAAAGAGGACACCGCGCTGTATGTGTGGCGACCGCGCAAGCTTGG 1200  
QY 1201 AGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGCGCGCACCAAGAGAGATGATGAGC 1260  
DB 1201 AGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGCGCGCACCAAGAGAGATGATGAGC 1260  
QY 1261 ACGAGCGCGAGCTGCTGATCAAGCAGGCTGCCAGTACGTGTGAGAGGCGCCCAATGC 1320  
DB 1261 ACGAGCGCGAGCTGCTGATCAAGCAGGCTGCCAGTACGTGTGAGAGGCGCCCAATGC 1320  
QY 1321 CTTTCAACAAAGAGGCGATCAAGTACAAAGAGCGCGGCAATCAATCAATCTGCGCGGCA 1380  
DB 1321 CTTTCAACAAAGAGGCGATCAAGTACAAAGAGCGCGGCAATCAATCAATCTGCGCGGCA 1380  
QY 1381 AGGCGGCAAGCGCGGCGGTGCGGCTCAGCGGCTGAGATGAGCCCAAGACGCAATGA 1440





QY 724 TGACGCGCCAGATCAGTACGTGACAGAGCGTCCCGCGCGACATCCGCGTGGCGCGC 783  
DB 721 TGACGCGCCAGATCAGTACGTGACAGAGCGTCCCGCGCGACATCCGCGTGGCGCGC 780  
QY 784 GCGAGATTGGCTACTCTTTTCGCGCAAGTACAAAGCATCAACAAAGTACACACCGCGTGC 843  
DB 781 GCGAGATTGGCTACTCTTTTCGCGCAAGTACAAAGCATCAACAAAGTACACACCGCGTGC 840  
QY 864 TGACCCCGAAGGCGGAGAGTATGGCGGCTCCGAGATCCCGCGCGACCGGCTACG 903  
DB 841 TGACCCCGAAGGCGGAGAGTATGGCGGCTCCGAGATCCCGCGCGACCGGCTACG 900  
QY 904 GCGCGCTGCTGTTTGTGAGAGAGTGTGAGAGAGCAAGAGGCGAGCGCTCAAGGCGAGC 963  
DB 901 GCGCGCTGCTGTTTGTGAGAGAGTGTGAGAGAGCAAGAGGCGAGCGCTCAAGGCGAGC 960  
QY 964 GCTGCTGTGTCTGTGGCGCGGCAAGTGTGCGCACTGCGCGAGCTGTGCTGAGAG 1023  
DB 961 GCTGCTGTGTCTGTGGCGCGGCAAGTGTGCGCACTGCGCGAGCTGTGCTGAGAG 1020  
QY 1024 AGGGGCGCATCTGT 1083  
DB 1021 AGGGGCGCATCTGT 1080  
QY 1084 TCACGCGCGAGCAGCTGTGAGGCGGTGACAGACATGAAGAGAGAGCAACAGCGCGCA 1143  
DB 1081 TCACGCGCGAGCAGCTGTGAGGCGGTGACAGACATGAAGAGAGAGCAACAGCGCGCA 1140  
QY 1144 TCTCCGAGTACAAAGAGCAGACACCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1203  
DB 1141 TCTCCGAGTACAAAGAGCAGACACCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200  
QY 1204 TGGAGCTGCAAGTGTGACATCGCTTCCCTGCGGCAACCAAGAGAGATTCAGTACGACG 1263  
DB 1201 TGGAGCTGCAAGTGTGACATCGCTTCCCTGCGGCAACCAAGAGAGATTCAGTACGACG 1260  
QY 1264 AGCGGAGCTGCTGTATCAAGCAGCGCTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1323  
DB 1261 AGCGGAGCTGCTGTATCAAGCAGCGCTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320  
QY 1324 CCACCAAGAGGCGCATTCACAAAGTACAAAGGCGCGCATCTTACTGCGCGCAAGG 1383  
DB 1321 CCACCAAGAGGCGCATTCACAAAGTACAAAGGCGCGCATCTTACTGCGCGCAAGG 1380  
QY 1384 CGGCGCAAGCGCGCGCGCTGCGGTGACGCGCTGAGAGATCCCAAGAGCGCATGAGCC 1443  
DB 1381 CGGCGCAAGCGCGCGCGCTGCGGTGACGCGCTGAGAGATCCCAAGAGCGCATGAGCC 1440  
QY 1444 TGAAGCTGAGCTCGGAGAGGTTGCGCAAGCTGTGAGCGCATCAATGAAGAGCATCTACG 1503  
DB 1441 TGAAGCTGAGCTCGGAGAGGTTGCGCAAGCTGTGAGCGCATCAATGAAGAGCATCTACG 1500  
QY 1504 ACTCGCGCATGCGGCGCTGCGCGAGATCAATGTGTGACCTGCGCGCGCGCAACATCG 1563  
DB 1501 ACTCGCGCATGCGGCGCTGCGCGAGATCAATGTGTGACCTGCGCGCGCGCAACATCG 1560  
QY 1564 CGGCGCTTACCAAGTGTGCTGATGCTGTGAGAGCGCGCAAGGCGCTGTGTTAACTGCGCAGG 1623  
DB 1561 CGGCGCTTACCAAGTGTGCTGATGCTGTGAGAGCGCGCAAGGCGCGCTGTGTTAACTGCGCAGG 1620  
QY 1624 CCAGAGCGAGGCTTACCGGCGCATTCACCAAGCGCGCAAGCGCGCGAGCGCTTTTGG 1683  
DB 1621 CCAGAGCGAGGCTTACCGGCGCATTCACCAAGCGCGCAAGCGCGCGAGCGCTTTTGG 1680  
QY 1684 AAGCGCGCGCTTTTCCAGCGCGAGCGCGCTTCACTGCGCTTTCATTAACCTGCTATTGCC 1743  
DB 1681 AAGCGCGCGCTTTTCCAGCGCGAGCGCGCTTCACTGCGCTTTCATTAACCTGCTATTGCC 1740  
QY 1744 GCGCGCGCGCTTTCATTCACCCCAAGAGAGAGTATGCGCGCATTCGATGCTACAGAGCGG 1803  
DB 1741 GCGCGCGCGCTTTCATTCACCCCAAGAGAGAGTATGCGCGCATTCGATGCTACAGAGCGG 1800  
QY 1804 CTATTTTTTGGCGAGCGCGCGCTACCGCGAGAGCGCTCTCTCCCGCGAGCGCTTAAGCGCT 1863

DB 1801 CTATTTTTTGGCGAGCGCGCTACCGCGAGAGCGCTCTCTCCCGAGCGCTTAAGCGCT 1860  
QY 1864 GACGTCCCGCGACTTTGCTGTGCAATCGCTCGGTTTGAACCCCTCTCACTTACCCAC 1923  
DB 1861 GACGTCCCGCGACTTTGCTGTGCAATCGCTCGGTTTGAACCCCTCTCACTTACCCAC 1920  
QY 1924 CCGTGTGAGAGCGCTTACAGTGAATGCGTTTGTAGTATGAGTGGCGCGCGCTCGCGCGC 1983  
DB 1921 CCGTGTGAGAGCGCTTACAGTGAATGCGTTTGTAGTATGAGTGGCGCGCGCTCGCGCGC 1980  
QY 1984 CGAATTTTCTGCGCATGAGAGTGTGCGGTTCTTACCTGTGTGACCCCAAGTAGAGTAACT 2043  
DB 1981 CGAATTTTCTGCGCATGAGAGTGTGCGGTTCTTACCTGTGTGACCCCAAGTAGAGTAACT 2040  
QY 2044 GTGCGTGTGCTGCGCTGCGCGCGTGTGCGGAGTGTGAGTGTGAGTGTGAGTGTGTA 2103  
DB 2041 GTGCGTGTGCTGCGCTGCGCGCGTGTGCGGAGTGTGAGTGTGAGTGTGAGTGTGTA 2100  
QY 2104 AACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140  
DB 2101 AACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2137

RESULT 4  
US-08-828-451-18  
; Sequence 18, Application US/08828451  
; Patent No. 5985634  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; APPLICANT: Miller, Philip  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanhik & Saliwanhik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,451  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,033  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UFI15  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2137 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; US-08-828-451-18

Query Match 99.9%; Score 2137; DB 2; Length 2137;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 CTTTCTGCTGCGCCCTCTCTCGCTCCCGCCATGACAGACCGCCCTGTCGCGCAAGCCTATCG 63  
1 CTTTCTGCTGCGCCCTCTCTCGCTCCCGCCATGACAGACCGCCCTGTCGCGCAAGCCTATCG 60  
64 TGGCCGCGCCCGCTGCGCGACCGCCGCTGCTCGCGCGCGCTGCGCGCTGCGCTGCGCTGCG 123  
61 TGGCCGCGCCCGCTGCGCGACCGCCGCTGCTGCGCGCGCTGCGCGCTGCGCTGCGCTGCG 120  
124 GCTCCGCGCAAGCGAGTGTCCGCGCGCAAGCGCGCTGCTGCGCGCGCTGCGCGCTGCGCG 183  
121 GCTCCGCGCAAGCGAGTGTCCGCGCGCAAGCGCGCTGCTGCGCGCGCTGCGCGCTGCGCG 180  
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181 TGAAGCGCACCGACCGCGCACTTCAAGCGCGCTGCGCGCGCTGCGCGCTGCGCGCAAGC 240  
244 AGCGCGGCGCATGAGGCGCTGCTGCGACCGCGCATCAAGAACCCCGACGTCGCGCTGCG 303  
241 AGCGCGGCGCATGAGGCGCTGCTGCGACCGCGCATCAAGAACCCCGACGTCGCGCTGCG 300  
304 CGGAGATCTTGAATGAAGGACCGGAGCGAGGAGTTGATGAGCGCGCTGCGCGAGGCTG 363  
301 CGGAGATCTTGAATGAAGGACCGGAGCGAGGAGTTGATGAGCGCGCTGCGCGAGGCTG 360  
364 CGGCTCCCTGCGACCGCGCTGCTGCGAGGAGCGCGCGCGCTGCGCGCTGCGCGCAAGC 423  
361 CGGCTCCCTGCGACCGCGCTGCTGCGAGGAGCGCGCGCGCTGCGCGCTGCGCGCAAGC 420  
424 TCGTTGAGCTGAGCGCGCTGATCACTTCGCGCTGCTGCGCTGCGCGCAAGC 483  
421 TCGTTGAGCTGAGCGCGCTGATCACTTCGCGCTGCTGCGCTGCGCGCAAGC 480  
484 TGAAGGTCAACCGCGCGCTGCGCGCGCTGCGCGCTGCGCGCGCTGCGCGCAAGC 543  
481 TGAAGGTCAACCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCAAGC 540  
544 GCTGCGCTGCGACCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCAAGC 603  
541 GCTGCGCTGCGACCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCAAGC 600  
604 TCTTCAAGAACCGCTGCGACCGCTGCGCGCGCTGCGCGCGCTGCGCGCAAGC 663  
601 TCTTCAAGAACCGCTGCGACCGCTGCGCGCGCTGCGCGCGCTGCGCGCAAGC 660  
664 ACGCCAGGCGGAGGAGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCAAGC 723  
661 ACGCCAGGCGGAGGAGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCAAGC 720  
724 TGAAGCGCGCATGAGCTGCGAGGAGCTGCGCGCGCGCGCGCATGCGCGCGCGCGCG 783  
721 TGAAGCGCGCATGAGCTGCGAGGAGCTGCGCGCGCGCGCGCATGCGCGCGCGCGCG 780  
784 GCGAGATTTGCTACCTTTTGGCGCGAGTACCAAGCGCATCAAGAACTCAACCGCGCTG 843  
781 GCGAGATTTGCTACCTTTTGGCGCGAGTACCAAGCGCATCAAGAACTCAACCGCGCTG 840  
844 TGAAGCGCGAAGGCGAGGAGTATGCGCGCGCTGCGAGTCCCGCGCGCGCGCGCGCTG 903  
841 TGAAGCGCGAAGGCGAGGAGTATGCGCGCGCTGCGAGTCCCGCGCGCGCGCGCGCTG 900  
904 GCGCGCTGCTGTTTGTGAGAACGTCGAAGGAGCAAGGCGAGGAGCTCAAGGCGCAAGC 963  
901 GCGCGCTGCTGTTTGTGAGAACGTCGAAGGAGCAAGGCGAGGAGCTCAAGGCGCAAGC 960  
964 GCTGCTGCTGCTGCTGCGCGCGCGCAAGCTGCGCGCATGCGCGCGAGCTGCTGCTGAG 1023  
961 GCTGCTGCTGCTGCTGCGCGCGCGCAAGCTGCGCGCATGCGCGCGAGCTGCTGCTGAG 1020  
1024 AGGCGCGCATGCTGCTGCTGCTGCGCGCGCATGCGCGCGCTGCTGCTGAGCGCGCGCT 1083  
1021 AGGCGCGCATGCTGCTGCTGCTGCGCGCGCATGCGCGCGCTGCTGCTGAGCGCGCGCT 1080

1084 TCAAGCGCGAGCACTGCGAGCGGTGCGAGGACATGAAGAAAGAACCAAGCGCGCGCA 1143  
1081 TCAAGCGCGAGCACTGCGAGCGGTGCGAGGACATGAAGAAAGAACCAAGCGCGCGCA 1140  
1144 TCTCCGAGTACAAAGAGGAGCAACCGCGCTGATATGTTGGCGCAACCGCGCAAGCTTGGAGC 1203  
1141 TCTCCGAGTACAAAGAGGAGCAACCGCGCTGATATGTTGGCGCAACCGCGCAAGCTTGGAGC 1200  
1204 TGAAGTGCAGAGTGAATGCGCGCTTCCCTGCGCGCAACCGAGAAAGGAGTGAAGAGC 1263  
1201 TGAAGTGCAGAGTGAATGCGCGCTTCCCTGCGCGCAACCGAGAAAGGAGTGAAGAGC 1260  
1264 ACGCGAGCTGCTGATCAAGCAAGCGCTGCGAGTACGTTGAGAGGCGCGCAAGCTG 1323  
1261 ACGCGAGCTGCTGATCAAGCAAGCGCTGCGAGTACGTTGAGAGGCGCGCAAGCTG 1320  
1324 CCACCAAGAGGCGCATCAAGTACAAAGAGCGCGCATCAATCTGCTGCGCGCAAGC 1383  
1321 CCACCAAGAGGCGCATCAAGTACAAAGAGCGCGCATCAATCTGCTGCGCGCAAGC 1380  
1384 CGGCGCAAGCGCGCGGTGCGCGCGGTGCGCGCGGTGCGAGTGAACCGCAAGCGCGAGC 1443  
1381 CGGCGCAAGCGCGCGGTGCGCGCGGTGCGCGCGGTGCGAGTGAACCGCAAGCGCGAGC 1440  
1444 TGAAGTGAAGTTCGCGAGAGGTTTCGCGCAAGCTGAGCGCATCAAGAGCACTTACG 1503  
1441 TGAAGTGAAGTTCGCGAGAGGTTTCGCGCAAGCTGAGCGCATCAAGAGCACTTACG 1500  
1504 ACTTCGCGCATGAGGCGCTTCCCGAGATACAAATGTTGACTGCTGCGCGCGCGCAAGCTG 1563  
1501 ACTTCGCGCATGAGGCGCTTCCCGAGATACAAATGTTGACTGCTGCGCGCGCGCAAGCTG 1560  
1564 CGGCGCTTCAAGAGTGGCTGATGCGCTCAAGGCGCGAGGCGCTGTTAAGCTGCGCGAG 1623  
1561 CGGCGCTTCAAGAGTGGCTGATGCGCTCAAGGCGCGAGGCGCTGTTAAGCTGCGCGAG 1620  
1624 CCCAAGCACGCGCTCACCGGCAATCCAAACCAACCAACTCAAGCGCGAGACCTTTTCG 1683  
1621 CCCAAGCACGCGCTCACCGGCAATCCAAACCAACCAACTCAAGCGCGAGACCTTTTCG 1680  
1684 AAGGCGCGCTTTTTCGAGCGAGGCGCTTCACTGCGCTTTTCAATACCTTGCATTTGCG 1743  
1681 AAGGCGCGCTTTTTCGAGCGAGGCGCTTCACTGCGCTTTTCAATACCTTGCATTTGCG 1740  
1744 GCGGTGCGCTGCAATTCGCAACCGCAAGAACTGAGGCGCACTTGAATGAGAGC 1803  
1741 GCGGTGCGCTGCAATTCGCAACCGCAAGAACTGAGGCGCACTTGAATGAGAGC 1800  
1804 CTATTTTTTTCGCGAGCGCGCTTCAACCGGAGAGCTCTTCCCGCGAGCCTTAAGCGCT 1863  
1801 CTATTTTTTTCGCGAGCGCGCTTCAACCGGAGAGCTCTTCCCGCGAGCCTTAAGCGCT 1860  
1864 GAGTCCGCGCGCACTTTGCTGCGCAATGCGTGGTTTTGACCCCGCTTCAAGCTTAC 1923  
1861 GAGTCCGCGCGCACTTTGCTGCGCAATGCGTGGTTTTGACCCCGCTTCAAGCTTAC 1920  
1924 CCGTGTGAGAGCTTACAGCTCAATGCGCTTTTGAAGTATGAGCGCGCGCTTCCGCGCG 1983  
1921 CCGTGTGAGAGCTTACAGCTCAATGCGCTTTTGAAGTATGAGCGCGCGCTTCCGCGCG 1980  
1984 CGAATTTTTCGCGCATGAGCTGCGGTTCTTACGCTGAGTGAACCGCAAGTGAAGT 2043  
1981 CGAATTTTTCGCGCATGAGCTGCGGTTCTTACGCTGAGTGAACCGCAAGTGAAGT 2040  
2044 GTGCTGCTTTCGCTGCGCTGCGCGGAGTGCATATCTGAGCTTGAAGTGTGCTTGTG 2103  
2041 GTGCTGCTTTCGCTGCGCTGCGCGGAGTGCATATCTGAGCTTGAAGTGTGCTTGTG 2100  
2104 AACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140  
2101 AACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2137







Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

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Oy 4 CTTTCTGTGCGCCCTCTCTCCGTCCCGCATGACAGACCGCCCTGCTGCGCAAGCCTATCG 63
Db 1 CTTTCTGTGCGCCCTCTCTCCGTCCCGCATGACAGACCGCCCTGCTGCGCAAGCCTATCG 60
Oy 64 TGCGCGCCCGCGTGGCGGACGCGCCGCGCTGCTGCGCGCGTGGCGCGTGGCTTC 123
Db 61 TGCGC-----TGCGCGTGGCTTC 78
Oy 124 GCTCCGCGCAAGCGGATGTCGCGCCGCAAGGCGGCTGCGCTGGAGAGAGAGATCTCCCGCA 183
Db 79 GCTCCGCGCAAGCGGATGTCGCGCCGCAAGGCGGCTGCTGGAGAGAGATCTCCCGCA 138
Oy 184 TGAGCGCCACCAACCGGCACTTCAAGCGCGCTGCAAGAAAGCGGTGAAGAGAGATGGCCACA 243
Db 139 TGAGAGCCACCAACCGGCACTTCAAGCGCGCTGCAAGAAAGCGGTGAAGAGATGGCCACA 198
Oy 244 AGCGGGGCACTGAGGGCGCTGGTGCACGGGATCAAGAAACCCGACGCTGGCCAGCTGTGTA 303
Db 199 AGCGGGGCACTGAGGGCGCTGGTGCACGGGATCAAGAAACCCGACGCTGTGTA 258
Oy 304 CCGAGATCTTATGAAGAACCCGGAGCGAGAGAGTTATGCAAGCGGTGGCGGAGGTGG 363
Db 259 CCGAGATCTTATGAAGAACCCGGAGCGAGAGAGTTATGCAAGCGGTGGCGGAGGTGG 318
Oy 364 CCGATCCCTGACCGCGCTGTTGAGAAAGCGCCCGAGCTGCTGCCATCTTCAAGCGA 423
Db 319 CCGATCCCTGACCGCGCTGTTGAGAAAGCGCCCGAGCTGCTGCCATCTTCAAGCGA 378
Oy 424 TCGTTGAGCCTGAGCGCGTGATCACTTCCGCGTGTCTGGCTGAGACGCGCGCAAC 483
Db 379 TCGTTGAGCCTGAGCGCGTGATCACTTCCGCGTGTCTGGCTGAGACGCGCGCAAC 438
Oy 484 TGGAGGTCAACCGGCGCTTCCGCGTGAGTACTGTCCGCGCATGGCGCCCTCAAGAGCG 543
Db 439 TGGAGGTCAACCGGCGCTTCCGCGTGAGTACTGTCCGCGCATGGCGCCCTCAAGAGCG 498
Oy 544 GCGTGCCTTCCACCCCTCCGTGAACCTGTCATCATGAATTCCTTGGCTTGAAGCA 603
Db 499 GCGTGCCTTCCACCCCTCCGTGAACCTGTCATCATGAATTCCTTGGCTTGAAGCA 558
Oy 604 TCTTCAAGAACAGCCTTGACACCCCTGCGATGGCGGCGGAGAGCGGCTCCGACTTTCG 663
Db 559 TCTTCAAGAACAGCCTTGACACCCCTGCGATGGCGGCGGAGAGAGCGGCTCCGACTTTCG 618
Oy 664 ACCCGAAGGGAAGAGCGACGCGAGGTGAGTGGCTTCTGCACTCTTCAATGAACGAGC 723
Db 619 ACCCGAAGGGAAGAGCGACGCGAGGTGAGTGGCTTCTGCACTCTTCAATGAACGAGC 678
Oy 724 TGACAGCGCATAGCTACGTGACGAGAGTGCCTCGCGCGGACATCGCGCTGGCGCGC 783
Db 679 TGACAGCGCATAGCTACGTGACGAGAGTGCCTCGCGCGGACATCGCGCTGGCGCGC 738
Oy 784 GCGAGATTGGCTACCTTTTGGGCGAGTACAAGCGCATCAACAAGAACTACAACGCGGTGC 843
Db 739 GCGAGATTGGCTACCTTTTGGGCGAGTACAAGCGCATCAACAAGAACTACAACGCGGTGC 798
Oy 844 TGACCGCGAAGGCGCAGAGATAGCGCGCTCCGAGATCCCGCCCGAGGCGCACCGGCTTACG 903
Db 799 TGACCGCGAAGGCGCAGAGATAGCGCGCTCCGAGATCCCGCCCGAGGCGCACCGGCTTACG 858
Oy 904 GCGCGGTGCTGTTTGTGAGAAAGTGTGAAGGACAAGAGCGAGAGCTCAAGGGCAAGC 963
Db 859 GCGCGGTGCTGTTTGTGAGAAAGTGTGAAGGACAAGAGCGAGAGCTCAAGGGCAAGC 918
Oy 964 GCTGCTGTGTGTGCGCGGCGCAACGTGGCCAGTACTGCGCGAGAGCTGTGCTGAGAGA 1023
Db 919 GCTGCTGTGTGTGCGCGGCGCAACGTGGCCAGTACTGCGCGAGAGCTGTGCTGAGAGA 978
Oy 1024 AGGGCGCATGTGTGCTGTGCTGCTGCACTCCAGGGCTTACGTGTACAGGCCCAACGGCT 1083
Db 979 AGGGCGCATGTGTGCTGTGCTGCTGCACTCCAGGGCTTACGTGTACAGGCCCAACGGCT 1038
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Oy 1084 TCAAGCGGAGCAGCTGCAAGCGGTGAGAGACATGAAAGAAAGAACAGCGCCCGCA 1143
Db 1039 TCAAGCGGAGCAGCTGCAAGCGGTGAGAGACATGAAAGAAAGAACAGCGCCCGCA 1098
Oy 1144 TCTCCGAGTACAAAGAGGACACCGCGCTGTATGTGGCGACCCGCGCAAGCTTTGGAGC 1203
Db 1099 TCTCCGAGTACAAAGAGGACACCGCGCTGTATGTGGCGACCCGCGCAAGCTTTGGAGC 1158
Oy 1204 TGACCTGCAAGGTGACATGCGCTTCCCTGCGGCAACCGAAGAGATGATGATGACG 1263
Db 1159 TGACCTGCAAGGTGACATGCGCTTCCCTGCGGCAACCGAAGAGATGATGATGACG 1218
Oy 1264 ACGCCGAGCTGTGATCAAGCAGGCTGCGAGTACGTGTGAGAGGGCGCAACATGCTT 1323
Db 1219 ACGCCGAGCTGTGATCAAGCAGGCTGCGAGTACGTGTGAGAGGGCGCAACATGCTT 1278
Oy 1324 CCACCAACGAGGCGCATCAAGTACAAAGAGCGCGCATCATCTACTGCGCCCGCAAG 1383
Db 1279 CCACCAACGAGGCGCATCAAGTACAAAGAGCGCGCATCATCTACTGCGCCCGCAAG 1338
Oy 1384 CCGCCAAAGCGCGGCGGTGGCGGTGAGCGGCGTGGATGACCCAGAACCGCATGAGCC 1443
Db 1339 CCGCCAAAGCGCGGCGGTGGCGGTGAGCGGCGTGGATGACCCAGAACCGCATGAGCC 1398
Oy 1444 TGAATGGAATCGGAGAGAGTTCGCGCAAGCTGAGCGCATCATGAAAGACATTTAC 1503
Db 1399 TGAATGGAATCGGAGAGAGTTCGCGCAAGCTGAGCGCATCATGAAAGACATTTAC 1458
Oy 1504 ACTCCGCAATGGGGCGCTCCCGCAGATACAAATGTTGACTGTGCGGGCGCCAACTCG 1563
Db 1459 ACTCCGCAATGGGGCGCTCCCGCAGATACAAATGTTGACTGTGCGGGCGCCAACTCG 1518
Oy 1564 CCGGCTTACCAAGAGTGTGATGCGGTCAAGGCGCAAGGCGGCTTTAAGCTGCGCCAG 1623
Db 1519 CCGGCTTACCAAGAGTGTGATGCGGTCAAGGCGGCGGCTTTAAGCTGCGCCAG 1578
Oy 1624 CCCAAGCCACGCGTCAACCGGCAATCCAAACCAACCACTCAACGCGCGAGACCTTTTCG 1683
Db 1579 CCCAAGCCACGCGTCAACCGGCAATCCAAACCAACCACTCAACGCGCGAGACCTTTTCG 1638
Oy 1684 AAGCGGCGCTTTTTCGAGCGAGGCGCTTCACTGCGCTTTTCAATACCTTGTCTATTGCC 1743
Db 1639 AAGCGGCGCTTTTTCGAGCGAGGCGCTTCACTGCGCTTTTCAATACCTTGTCTATTGCC 1698
Oy 1744 GCGGTGCCCTGCAATTCCACCCCAAGAAAGACTGAGCGGCACTGATCAGAGAGC 1803
Db 1699 GCGGTGCCCTGCAATTCCACCCCAAGAAAGACTGAGCGGCACTGATCAGAGAGC 1758
Oy 1804 CTATTTTTCGCGACGCGGCTTCAACCGAGAGCTCTCTCCCGAGGCTTAAGCGCT 1863
Db 1759 CTATTTTTCGCGACGCGGCTTCAACCGAGAGCTCTCTCCCGAGGCTTAAGCGCT 1818
Oy 1864 GAGGTCCCGGCACTTTGCTCGGCAATGCGTGGTTTTTGAACCCCTCCAGTCAACCA 1923
Db 1819 GAGGTCCCGGCACTTTGCTCGGCAATGCGTGGTTTTTGAACCCCTCCAGTCAACCA 1878
Oy 1924 CCGTGTGAAGCTTACAGCTCAATGCGCTTTAAGTATGTGCGGCGCCCTCTGCGCC 1983
Db 1879 CCGTGTGAAGCTTACAGCTCAATGCGCTTTAAGTATGTGCGGCGCCCTCTGCGCC 1938
Oy 1984 CGAATTTTCGCGCATGAGAGTGGCGGTTCTAGCTGTGACCCCAAGTAGCATTAGT 2043
Db 1939 CGAATTTTCGCGCATGAGAGTGGCGGTTCTAGCTGTGACCCCAAGTAGCATTAGT 1998
Oy 2044 GTGCGTCCCTTGGCGCTGCGCTCCCGGAGTGCATCTGTGACTGAGAGTCTTGTGTA 2103
Db 1999 GTGCGTCCCTTGGCGCTGCGCTCCCGGAGTGCATCTGTGACTGAGAGTCTTGTGTA 2058
Oy 2104 AACGAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140
Db 2059 AACGAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2095
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OY	1444	TGAATCGAATCGGAGAGAGGTTGGCCGCAAGCTGAGACCGGATCATGTAAGACATCTACG	1503
Db	1399	TGAATCGAATCGGAGAGAGGTTGGCCGCAAGCTGAGAGCGATCATGTAAGACATCTACG	1458
OY	1504	ACTCCGCGCATGGGGCCGTCCCGCAGATACAAATGTTGACCTTGCGTGGGGCCGCAACATCG	1563
Db	1459	ACTCCGCGCATGGGGCCGTCCCGCAGATACAAATGTTGACCTTGCGTGGGGCCGCAACATCG	1518
OY	1564	CGGGCTTACCAAGGTGGCTGATGCGGCAAGGGCCAGGGGGCGTGTTAAGCTGCCACG	1623
Db	1519	CGGGCTTACCAAGGTGGCTGATGCGGCAAGGGCCAGGGGGCGTGTTAAGCTGCCACG	1578
OY	1624	CCCAAGCCACGGCTCACCGGCAATCCAAACCAACCTCAACGGCCACGACCTTTTCGG	1683
Db	1579	CCCAAGCCACGGCTCACCGGCAATCCAAACCAACCTCAACGGCCACGACCTTTTCGG	1638
OY	1684	AAGGGGGGCGCTTTTCCAGGCAAGGGCCCTCACCTGGCCCTTTCATTAACCTCGCTATTGGC	1743
Db	1639	AAGGGGGGCGCTTTTCCAGGCAAGGGCCCTCACCTGGCCCTTTCATTAACCTCGCTATTGGC	1698
OY	1744	GCCGTGCCCTCTGCAATTTCCACCCCAAGAAAGACTAGCGGCACTTGACCTGCATCAGACGG	1803
Db	1699	GCCGTGCCCTCTGCAATTTCCACCCCAAGAAAGACTAGCGGCACTTGACCTGCATCAGACGG	1758
OY	1804	CTATTTTTTTTTGGCAAGCGCGCTCACCCCGAAGAGCTCTCTCCGCCGACTTAAGCGCT	1863
Db	1759	CTATTTTTTTTTGGCAAGCGCGCTCACCCCGAAGAGCTCTCTCCGCCGACTTAAGCGCT	1818
OY	1864	GACGTCGCGCCGACCTTTCCTGCGACATCGCTCGGTTTTGACCCCTCAGACTTAACCGAC	1923
Db	1819	GACGTCGCGCCGACCTTTCCTGCGACATCGCTCGGTTTTGACCCCTCAGACTTAACCGAC	1878
OY	1924	CTGTGTGTGAAGCCTACCAAGCTCAATTGCTTTTATGTATGTGTGGCCCTCTCGTCC	1983
Db	1879	CTGTGTGTGAAGCCTACCAAGCTCAATTGCTTTTATGTATGTGTGGCCCTCTCGTCC	1938
OY	1984	GGAATTTTCCAGCATGAGAGGTGGGTTCTTAGCGCTGTACCCCAAGTACGATTAGT	2043
Db	1939	GGAATTTTCCAGCATGAGAGGTGGGTTCTTAGCGCTGTACCCCAAGTACGATTAGT	1998
OY	2044	GTGCGTGCCTTTCGCTGCGCTGCCCGGAGTCGATACCTGTGACCTGAGAGTCTTGTTGA	2103
Db	1999	GTGCGTGCCTTTCGCTGCGCTGCCCGGAGTCGATACCTGTGACCTGAGAGTCTTGTTGA	2058
OY	2104	AACACGACGATCAAAAAAAAAAAAAAAAAAAAAA 2140	
Db	2059	AACACGACGATCAAAAAAAAAAAAAAAAAAAAAA 2095	

RESULT 9  
 US-08-541-033A-7  
 Sequence 7, Application US/08541033A  
 Patent No. 5878941  
 GENERAL INFORMATION:  
 APPLICANT: Schmidt, Robert R.  
 APPLICANT: Miller, Philip  
 TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
 TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
 TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Saliwanchik & Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: Florida  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/541,033A
3 FILING DATE:
4
5 CLASSIFICATION: 435
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Whillock, Ted W.
8 REGISTRATION NUMBER: 36,965
9 REFERENCE/DOCKET NUMBER: U1155
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (904) 375-8100
12 TELEFAX: (904) 372-5800
13 INFORMATION FOR SEQ ID NO: 7:
14
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 1969 base pairs
17 TYPE: nucleic acid
18 STRANDEDNESS: double
19 TOPOLOGY: linear
20 MOLECULE TYPE: CDNA
21
22 US-08-541-033A-7

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92.0%; Score 1969; DB 2; Length 1969;	
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1969; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	171 CAGATCTCCGGATGACGCCACCAACCGGCGACTTCAACGCGCTGCGAGAAAGCGGTGAAG 230
Db	1 CAGATCTCCGGATGAGAGCCACCAACCGGCGACTTCAACGCGCTGCGAGAAAGCGGTGAAG 60
QY	231 CAGATGCGCAACGAGGGGGGACCTGAGGCGCTGGTGCACGGGCATCAAGAACCCCGAGGTG 290
Db	61 CAGATGCGCAACGAGGGGGGACCTGAGGCGCTGGTGCACGGGCATCAAGAACCCCGAGGTG 120
QY	291 CGCAGCGTGTGACCGGAGATCTTATGATGAAGACCGGAGCAGCAGAGATTATGACAGCG 350
Db	121 CGCAGCGTGTGACCGGAGATCTTATGATGAAGACCGGAGCAGCAGAGATTATGACAGCG 180
QY	351 GTGCGCAGAGTGCCTGCTCCCTGACGCGCTGTTGAAAGAGCCGCCGAGCTGCTGCC 410
Db	181 GTGCGCAGAGTGCCTGCTCCCTGACGCGCTGTTGAAAGAGCCGCCGAGCTGCTGCC 240
QY	411 ATCTTCAAGCAGATCTGTTGAGCCCTGAGCGGTATACACTTCCTCGCGTCTGCGCTGAC 470
Db	241 ATCTTCAAGCAGATCTGTTGAGCCCTGAGCGGTATACACTTCCTCGCGTCTGCGCTGAC 300
QY	471 GAGCGCGGCAACTGCAAGTCAACCGCGGCTTCGCGCTGCACTGCTCCGCATCGCG 530
Db	301 GAGCGCGGCAACTGCAAGTCAACCGCGGCTTCGCGCTGCACTGCTCCGCATCGCG 360
QY	531 CCTTACAAGGGGGCGCTGCGCTTCAACCCCTCCGTGAACCTGTTCATCATGAAGTTCTT 590
Db	361 CCTTACAAGGGGGCGCTGCGCTTCAACCCCTCCGTGAACCTGTTCATCATGAAGTTCTT 420
QY	591 GCGTTAGACGATCTTCAAGAACGCTGACACCCCTGGGCCATGAGGGGGGCAAGGGC 650
Db	421 GCGTTAGACGATCTTCAAGAACGCTGACACCCCTGGGCCATGAGGGGGGCAAGGGC 480
QY	651 GGCTCCGACTTGCACCCCAAGGGGCAAGGCGCAGAGTGTGCGCTTTCGCCAGTCC 710
Db	481 GGCTCCGACTTGCACCCCAAGGGGCAAGGCGCAGAGTGTGCGCTTTCGCCAGTCC 540
QY	711 TTCAATGACCGAGCTGACGCGCCACATCACTGACGAGCATGTGCCCGCGGCAATC 770
Db	541 TTCAATGACCGAGCTGACGCGCCACATCACTGACGAGCATGTGCCCGCGGCAATC 600
QY	771 GGCGTGGGCGGGCGAGATTGGGCTACTTTTCGGCCAGTACAAGCGCATACCAAGAAC 830
Db	601 GGCGTGGGCGGGCGAGATTGGGCTACTTTTCGGCCAGTACAAGCGCATACCAAGAAC 660
QY	831 TACACCGGCGTGTGACCCCGAAGGGCGCAGAGTATGGCGGCTCGAGATCCGCCCGAG 890
Db	661 TACACCGGCGTGTGACCCCGAAGGGCGCAGAGTATGGCGGCTCGAGATCCGCCCGAG 720
QY	891 GCCACCGGCTTACGGGCGCGTCTGTTGTGTGAAACGTGCTGAAGAGACAGGGCGAGAGC 950



QY 351 GTGCGAGAGTGACGCTTCCTGACAGCCGCTGTTGAGAAAGCCGCCGAGCTCTGCCC 410  
 Db 181 GTGCGAGAGTGACGCTTCCTGACAGCCGCTGTTGAGAAAGCCGCCGAGCTCTGCCC 240  
 QY 411 ATCTTCAAGAGATGCTTGAAGCTGAGGCGCTGATCACTTCCCGCTGCTCTGCTGGAC 470  
 Db 241 ATCTTCAAGAGATGCTTGAAGCTGAGGCGCTGATCACTTCCCGCTGCTCTGCTGGAC 300  
 QY 471 GAGCGCGGCAACCTGAGAGTCAACCGCGGCTTCCGCGTGAAGTACTGTCGCGCATGAGC 530  
 Db 301 GAGCGCGGCAACCTGAGAGTCAACCGCGGCTTCCGCGTGAAGTACTGTCGCGCATGAGC 360  
 QY 531 CCCTACAAGAGGCGGCTGCGCTTCAACCCCTCGTGAACCTGTCCATCATGAAGTTCCTT 590  
 Db 361 CCCTACAAGAGGCGGCTGCGCTTCAACCCCTCGTGAACCTGTCCATCATGAAGTTCCTT 420  
 QY 591 GCTTTGAGAGATCTTCAAGAACAGCTTGAACCTGCGCCATGAGGCGGCGGCAAGGCG 650  
 Db 421 GCTTTGAGAGATCTTCAAGAACAGCTTGAACCTGCGCCATGAGGCGGCGGCAAGGCG 480  
 QY 651 GGTCCGACTTGAACCCCAAGGCAAGAGCGAGGAGTGAAGTGGCTTCTGCGAGTCC 710  
 Db 481 GGTCCGACTTGAACCCCAAGGCAAGAGCGAGGAGTGAAGTGGCTTCTGCGAGTCC 540  
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 QY 771 GGGCTGGGCGCGCGAGATTTGGCTACCTTTTGGCGCATGACAGCGCATATCAAGAAC 830  
 Db 601 GGGCTGGGCGCGCGAGATTTGGCTACCTTTTGGCGCATGACAGCGCATATCAAGAAC 660  
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 Db 661 TACACCGGCGTGTGACCCCGAAGGAGAGATATGAGCGGCTCGAGATCCGCGCGAG 720  
 QY 891 GCGACCGGCTTACGCGCGCTGCTGTTTGTGAGAACGCTGTGAAGAACAGAGGCGAGAGC 950  
 Db 721 GCGACCGGCTTACGCGCGCTGCTGTTTGTGAGAACGCTGTGAAGAACAGAGGCGAGAGC 780  
 QY 951 CTCAAGGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1010  
 Db 781 CTCAAGGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
 QY 1011 CTGCTGCTGAGAGAGGAGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070  
 Db 841 CTGCTGCTGAGAGAGGAGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
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 Db 901 GAGCGCAACGCGCTTACGCGCGGAGAGCTGAGAGCGGCTGAGAGCATGAAGAGAGAAC 960  
 QY 1131 AACGCGCGCGCATCTCCGAGATCAAGAGCGACCCGCGTGTATGTGGGCGACCCGCGC 1190  
 Db 961 AACGCGCGCGCATCTCCGAGATCAAGAGCGACCCGCGTGTATGTGGGCGACCCGCGC 1020  
 QY 1191 AAGCGTTGGAGAGTGAAGTGCAGAGTGAAGATGCGCTTCCCTGCGCGACCCAGAGAGAG 1250  
 Db 1021 AAGCGTTGGAGAGTGAAGTGCAGAGTGAAGATGCGCTTCCCTGCGCGACCCAGAGAGAG 1080  
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 Db 1081 ATTCATGAGAGAGAGCGCGAGCTGATCAAGAGCGGCTGACAGATGCTGAGAGAGAGC 1140  
 QY 1311 GCGCAATGCGCTTCAACCAAGAGGCGCATCAAGATGCAAGAGGCGCGGATCATCTAC 1370  
 Db 1141 GCGCAATGCGCTTCAACCAAGAGGCGCATCAAGATGCAAGAGGCGCGGATCATCTAC 1200  
 QY 1371 TGCGCGCGAGAGGCGCGCAAGCGCGGCGGCTGAGCGGCTGAGAGATGAGAGAGCAG 1430  
 Db 1201 TGCGCGCGAGAGGCGCGCAAGCGCGGCGGCTGAGCGGCTGAGAGATGAGAGAGCAG 1260  
 QY 1431 AACCGCATGAGCTGAATCTGAGCTGCGAGAGAGGTTCCGCAAGAGCTGAGCGCATATG 1490

Db 1261 AACCGCATGAGCTGAATCTGAGCTGCGAGAGAGTTCCAGCAAGCTGAGCGCATATG 1320  
 QY 1491 AAGGACATTCAGCATCCGCGCATGAGGCGGCTCCGCGAGATACATATGACTGAGCTGCG 1550  
 Db 1321 AAGGACATTCAGCATCCGCGCATGAGGCGGCTCCGCGAGATACATATGACTGAGCTGCG 1380  
 QY 1551 GAGCGCAACATCGCGGCTTCAACCAAGTGAAGTGCCTGCAAGGCGGCGCTGTT 1610  
 Db 1381 GAGCGCAACATCGCGGCTTCAACCAAGTGAAGTGCCTGCAAGGCGGCGCTGTT 1440  
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 Db 1441 TAAGCTGCCAGGCGCCAGGCGCATGAGCTCACCGGCAATCCAACTCAAGAGGCGC 1500  
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 QY 1731 CCTGCTATTGCGCGCGCTGCGCTGCAATTCACCCCAAGAGAACTAGCGGCACTTGAC 1790  
 Db 1561 CCTGCTATTGCGCGCGCTGCGCTGCAATTCACCCCAAGAGAACTAGCGGCACTTGAC 1620  
 QY 1791 TGATCAAGAGCGCTATTTTTCGCGAGCGGCGCTCAACCCGAGAGCTCTCTCCCG 1850  
 Db 1621 TGATCAAGAGCGCTATTTTTCGCGAGCGGCGCTCAACCCGAGAGCTCTCTCCCG 1680  
 QY 1851 AGGCGTAAGGCTGAGAGCTGCGCGCGAGCTTTCCTGCGAGATGCTGCTGTTGAGCCCT 1910  
 Db 1681 AGGCGTAAGGCTGAGAGCTGCGCGCGAGCTTTCCTGCGAGATGCTGCTGTTGAGCCCT 1740  
 QY 1911 CCACTACACCACTGCTGTGAGAGCTACAGCTCAATTCCTTTAGTATGATGTCGC 1970  
 Db 1741 CCACTACACCACTGCTGTGAGAGCTACAGCTCAATTCCTTTAGTATGATGTCGC 1800  
 QY 1971 CCGCTCTGCGCGCGAATTTTCTGCGCATGAGAGCTGCTGCTGCTGCTGCTGCTGCTG 2030  
 Db 1801 CCGCTCTGCGCGCGAATTTTCTGCGCATGAGAGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
 QY 2031 AGTAGAGATTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2090  
 Db 1861 AGTAGAGATTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920  
 QY 2091 GAGTGTCTGTGTAACAAGAGCTCAAAAAAAAAAAAAAAAAAAAAA 2139  
 Db 1921 GAGTGTCTGTGTAACAAGAGCTCAAAAAAAAAAAAAAAAAAAAAA 1969

RESULT 11  
 US-08-541-033A-23  
 : Sequence 23, Application US/08541033A  
 : Patent No. 5879941  
 : GENERAL INFORMATION:  
 : APPLICANT: Schmidt, Robert R.  
 : APPLICANT: Miller, Philip  
 : TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
 : TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE  
 : TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
 : NUMBER OF SEQUENCES: 26  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Saliwanchik & Saliwanchik  
 : STREET: 2421 N.W. 41st Street, Suite A-1  
 : CITY: Gainesville  
 : STATE: Florida  
 : COUNTRY: USA  
 : ZIP: 32606  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/541, 033A

FILED DATE: 435  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1506 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 4..1464  
US-08-541-033A-23

Query Match 70.2%; Score 1501.4; DB 2; Length 1506;  
Best Local Similarity 99.9%; Pred. No. 1.8e-295;  
Matches 1502; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 150 AAGGCGCTGCTGAGGAGAGACATCTCCGAGATGAGCGGACACCGGAGCCTTCACG 209  
DB 4 ATGGCCGCTGCTGAGGAGAGACATCTCCGAGATGAGCGGACACCGGAGCCTTCACG 63  
QY 210 GCGCTGAGAGAGGCGGTGAACAGATGAGCCACCAAGCGGCGACCTGAGGCGTGCAC 269  
DB 64 GCGCTGAGAGAGGCGGTGAACAGATGAGCCACCAAGCGGCGACCTGAGGCGTGCAC 123  
QY 270 GGCATCAAGAACCCCGAGCTGCGGACGCTGCTGACCGAGATCTTCATGAAGACCCGAG 329  
DB 124 GGCATCAAGAACCCCGAGCTGCGGACGCTGCTGACCGAGATCTTCATGAAGACCCGAG 183  
QY 330 CAGAGAGAGTCAATGAGGCGGCGGTGCGGAGTGGCGGCTTCCTCCGAGCCGCTGTTGAG 389  
DB 184 CAGAGAGAGTCAATGAGGCGGCGGTGCGGAGTGGCGGCTTCCTCCGAGCCGCTGTTGAG 243  
QY 390 AAGCGCCCGAGCTGCTGCCATCTTCAGAGAGATGTTGAGCGCTGAGCGGTGATCAC 449  
DB 244 AAGCGCCCGAGCTGCTGCCATCTTCAGAGAGATGTTGAGCGCTGAGCGGTGATCAC 303  
QY 450 TTCGCGGTGCTGCTGAGAGAGCGGCGCACTGAGAGTCAACCGGCGCTTCGCGGTG 509  
DB 304 TTCGCGGTGCTGCTGAGAGAGCGGCGCACTGAGAGTCAACCGGCGCTTCGCGGTG 363  
QY 510 CAGTACTGCTCCGCGCATGCGGCGCTTCAAGAGGCGGCGCTTCACCCCTCCGTGAG 569  
DB 364 CAGTACTGCTCCGCGCATGCGGCGCTTCAAGAGGCGGCGCTTCACCCCTCCGTGAG 423  
QY 570 CTGTCCATCATGAGATCTCTGCTTGAAGAGATCTTCAGAGACAGCTGACCACTTCG 629  
DB 424 CTGTCCATCATGAGATCTCTGCTTGAAGAGATCTTCAGAGACAGCTGACCACTTCG 483  
QY 630 CCCATGAGCGGCGGCAAGGCGGCTCCGACTTCGACCCCAAGGCGCAAGAGCGGAG 689  
DB 484 CCCATGAGCGGCGGCAAGGCGGCTCCGACTTCGACCCCAAGGCGCAAGAGCGGAG 543  
QY 690 GTGATGCGCTTTCGCGCATCTTCATGACCGAGCTGACGCGGCGCATGACCTGACG 749  
DB 544 GTGATGCGCTTTCGCGCATCTTCATGACCGAGCTGACGCGGCGCATGACCTGACG 603  
QY 750 GACGTGCGGCGGCGGAGCATGCGGCTGAGCGGCGGAGATGAGTTCCTTTGCGGCGAG 809  
DB 604 GACGTGCGGCGGCGGAGCATGCGGCTGAGCGGCGGAGATGAGTTCCTTTGCGGCGAG 663  
QY 810 TACAAGCGCATCACCAAGAACTACACCGGCGTGTGACCCCGAAGGCGGCGAGATATGCG 869  
DB 664 TACAAGCGCATCACCAAGAACTACACCGGCGTGTGACCCCGAAGGCGGCGAGATATGCG 723

QY 870 GGCTCCGAGATCCGCCCGGAGGCGCACCGGCTACCGGCGCGCTGCTGTTGTGAGAACGTG 929  
DB 724 GGCTCCGAGATCCGCCCGGAGGCGCACCGGCTACCGGCGCGCTGCTGTTGTGAGAACGTG 783  
QY 930 CTGAAGGACCAAGGCGGAGAGCTTCAGAGGCGCAAGCGCTGCTGCTGCTGCGGCGGAC 989  
DB 784 CTGAAGGACCAAGGCGGAGAGCTTCAGAGGCGCAAGCGCTGCTGCTGCTGCGGCGGAC 843  
QY 990 GTGCGCCAGTACTGCGGCGGAGCTGCTGCTGCTGAGAGAGGCGGCGCATCTGCTGCTGCTG 1049  
DB 844 GTGCGCCAGTACTGCGGCGGAGCTGCTGCTGCTGAGAGAGGCGGCGCATCTGCTGCTGCTG 903  
QY 1050 GACTCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1109  
DB 904 GACTCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 963  
QY 1110 CAGGACATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1169  
DB 964 CAGGACATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1023  
QY 1170 GTGATGCGGCGGAGCGGCGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1229  
DB 1024 GTGATGCGGCGGAGCGGCGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
QY 1230 CCTGCGCGCAACCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1289  
DB 1084 CCTGCGCGCAACCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143  
QY 1290 TGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1349  
DB 1144 TGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203  
QY 1350 AACAGGCGCGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1409  
DB 1204 AACAGGCGCGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263  
QY 1410 AGCGGCGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1469  
DB 1264 AGCGGCGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323  
QY 1470 GACAGCTGAGAGCGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1529  
DB 1324 GACAGCTGAGAGCGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383  
QY 1530 TACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1589  
DB 1384 TACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1443  
QY 1590 GTCAAGGCGGAGGCGGCTGTTTAAAGTCCGAGGCGCAAGCGGCTCACCGGCAATCC 1649  
DB 1444 GTCAAGGCGGAGGCGGCTGTTTAAAGTCCGAGGCGCAAGCGGCTCACCGGCAATCC 1503  
QY 1650 AAC 1652  
DB 1504 AAC 1506

RESULT 12  
US-08-451-23  
Sequence 23, Application US/08828451  
Patent No. 5985634  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND - SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanhik & Saliwanhik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida

COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,451  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1506 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 4..1464  
US-08-828-451-23

Query March 70.2%; Score 1501.4; DB 2; Length 1506;  
Bee local Similarity 99.9%; Pred. No. 1.8e-295;  
Matches 1502; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 150 AAGCCGCTGCTGCTGAGAGAGATCTCCGAGTGAAGCCACCAACCGGAGCTTCAAG 209  
DB 4 ATGGCCGCTGCTGCTGAGAGAGATCTCCGAGTGAAGCCACCAACCGGAGCTTCAAG 63  
QY 210 GCGCTGAGAGAGCGGCTGAGAGATGAGCAACCAAGCGGAGCTGAGAGCGCTGAGAC 269  
DB 64 GCGCTGAGAGAGCGGCTGAGAGATGAGCAACCAAGCGGAGCTGAGAGCGCTGAGAC 123  
QY 270 GGCATCAAGAACCCCGAGCTGAGCGGAGCTGAGCGGAGCTTCAAGAGAGAGAGAG 329  
DB 124 GGCATCAAGAACCCCGAGCTGAGCGGAGCTGAGCGGAGCTTCAAGAGAGAGAGAG 183  
QY 330 CAGCAGAGATTCATGAGAGCGGAGCTGAGCGGAGCTTCAAGAGAGAGAGAGAG 389  
DB 184 CAGCAGAGATTCATGAGAGCGGAGCTGAGCGGAGCTTCAAGAGAGAGAGAGAG 243  
QY 390 AAGCGCCCGAGCTGAGCGGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 449  
DB 244 AAGCGCCCGAGCTGAGCGGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 303  
QY 450 TTCCGCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 509  
DB 304 TTCCGCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363  
QY 510 CAGTACTGCTCGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 569  
DB 364 CAGTACTGCTCGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423  
QY 570 CTGTCCATCATGAAGTTCTTTCCTTTGAGAGAGATCTTCAAGAGAGAGAGAGAG 629  
DB 424 CTGTCCATCATGAAGTTCTTTCCTTTGAGAGAGATCTTCAAGAGAGAGAGAGAG 483  
QY 630 CCCTATGAG 689  
DB 484 CCCTATGAG 543

QY 690 GTGATGCGCTTTCGAGTCTTCATGACCGAGCTGAGGCGCAATCAGCTACGTGAG 749  
DB 544 GTGATGCGCTTTCGAGTCTTCATGACCGAGCTGAGGCGCAATCAGCTACGTGAG 603  
QY 750 GAGTGTCCCGCGGAGCATTCGGGCTGAGGCGGCGGAGAGTTGGCTACCTTTCCGGCAG 809  
DB 604 GAGTGTCCCGCGGAGCATTCGGGCTGAGGCGGCGGAGAGTTGGCTACCTTTCCGGCAG 663  
QY 810 TACAAGGCGATCAACCAAGACTACACCGGAGTGTGACCCCGAAGGCGCAGAGTATGCG 869  
DB 664 TACAAGGCGATCAACCAAGACTACACCGGAGTGTGACCCCGAAGGCGCAGAGTATGCG 723  
QY 870 GGCCTCCGAGATCCGCGCGAGGAGCCACCGGCTACCGGCGCTGTTTGTGAGAACGTG 929  
DB 724 GGCCTCCGAGATCCGCGCGAGGAGCCACCGGCTACCGGCGCTGTTTGTGAGAACGTG 783  
QY 930 CTGAAGAGCAAGGCGGAGAGCTTCAAGAGGAGAACCGCTGCTGCTGCTGCTGCTGCTG 989  
DB 784 CTGAAGAGCAAGGCGGAGAGCTTCAAGAGGAGAACCGCTGCTGCTGCTGCTGCTGCTG 843  
QY 990 GTGGCCCACTATGCGCGGAGCTGCTGCTGAGAGAGAGGCGCAATCGTGTGCTGCTGCTG 1049  
DB 844 GTGGCCCACTATGCGCGGAGCTGCTGCTGAGAGAGAGGCGCAATCGTGTGCTGCTGCTG 903  
QY 1050 GACTCCAGGAGCTACGTGTAAGAGCCCAAGGCTTCAAGGCGAGAGCTGAGAGCGGTG 1109  
DB 904 GACTCCAGGAGCTACGTGTAAGAGCCCAAGGCTTCAAGGCGAGAGCTGAGAGCGGTG 963  
QY 1110 CAGGACATGAAG 1169  
DB 964 CAGGACATGAAG 1023  
QY 1170 GTGATGTGGGCGAGCGCGCAAGGCTTGGAGAGTGGAGCTGCGAGGAGTACATGCGCTTC 1229  
DB 1024 GTGATGTGGGCGAGCGCGCAAGGCTTGGAGAGTGGAGCTGCGAGGAGTACATGCGCTTC 1083  
QY 1230 CCTGTGCGCACCCAGAAAGAGATGATGAGACAGCGCGAGCTGTGATCAAGACGCGC 1289  
DB 1084 CCTGTGCGCACCCAGAAAGAGATGATGAGACAGCGCGAGCTGTGATCAAGACGCGC 1143  
QY 1290 TGCCTAGTACGTGTGAGAGGCGCGCAATGCTCTCCACCAAGAGGCAATCCCAAGTAC 1349  
DB 1144 TGCCTAGTACGTGTGAGAGGCGCGCAATGCTCTCCACCAAGAGGCAATCCCAAGTAC 1203  
QY 1350 AACCAAGGCGCGCATCATCTACTGCGCGGAGAGGCGCAAGCGGCGGCGTGC 1409  
DB 1204 AACCAAGGCGCGCATCATCTACTGCGCGGAGAGGCGCAAGCGGCGGCGTGC 1263  
QY 1410 AGCGGCTGAGAGTACCCAGAACCGGATGAGCTGAACTGGAAGTGGAGAGTTCGC 1469  
DB 1264 AGCGGCTGAGAGTACCCAGAACCGGATGAGCTGGAAGTGGAGAGTTCGC 1323  
QY 1470 GACAGCTGAGAGGCGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1529  
DB 1324 GACAGCTGAGAGGCGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1283  
QY 1530 TACAAGTTGACCTGAGTGGGCGGCGCAATGCGGAGCTTCAAGAGTGGCTGATGCC 1589  
DB 1384 TACAAGTTGACCTGAGTGGGCGGCGCAATGCGGAGCTTCAAGAGTGGCTGATGCC 1443  
QY 1590 GTCAGAGCCCAAGGCGCTGTTTAAAGTGCACAGGCGCAAGCCAGGCTCACCGCAATCC 1649  
DB 1444 GTCAGAGCCCAAGGCGCTGTTTAAAGTGCACAGGCGCAAGCCAGGCTCACCGCAATCC 1503  
QY 1650 AAC 1652  
DB 1504 AAC 1506

RESULT 13  
US-08-541-033A-25  
; Sequence 25, Application US/08541033A  
; Patent No. 5879941



GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE "- AND -SUBUNITS OF GLUTAMATE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1473 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 4..1431  
US-08-541-033A-25

Query Match 68.7%; Score 1470; DB 2; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 4.1e-289;  
Matches 1470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 ATGACGCGCACCGCGGCACTTCAAGCGCTGCGAGAGCGGTGAAGAGATGCGCCACC 242  
DB 4 ATGACGCGCACCGCGGCACTTCAAGCGCTGCGAGAGCGGTGAAGAGATGCGCCACC 63  
QY 243 AAGCGGCGCACTGAGGCGCTGTGTCACGCGCATCAAGAACCCCGACGTGCGCCAGCTGCTG 302  
DB 64 AAGCGGCGCACTGAGGCGCTGTGTCACGCGCATCAAGAACCCCGACGTGCGCCAGCTGCTG 123  
QY 303 ACCGAGATCTTCATGAAGAGACCGCGAGAGAGAGATTCATGACAGCGCGGTGCGAGAGTG 362  
DB 124 ACCGAGATCTTCATGAAGAGACCGCGAGAGAGAGATTCATGACAGCGCGGTGCGAGAGTG 183  
QY 363 GCCGCTCTCTGACAGCGCGGTGTCAGAGAGCGCGCGAGCTGCTGCCATCTTCAAGCAG 422  
DB 184 GCCGCTCTCTGACAGCGCGGTGTCAGAGAGCGCGCGAGCTGCTGCCATCTTCAAGCAG 243  
QY 423 ATCGTTGAGCTGAGCGCGGTGATCACTTCCGCGGTGCTGTGTCGAGAGCGCGCGCAAC 482  
DB 244 ATCGTTGAGCTGAGCGCGGTGATCACTTCCGCGGTGCTGTGTCGAGAGCGCGCGCAAC 303  
QY 483 CTGCAAGTCAACCGCGGCTTCGCGGTGATCACTGTCGCGCATGAGCGCGCTTCAAGAGGC 542  
DB 304 CTGCAAGTCAACCGCGGCTTCGCGGTGATCACTGTCGCGCATGAGCGCGCTTCAAGAGGC 363  
QY 543 GCGCTGCGCTTCAACCGCTTCAAGCTGTCATCATGAAGTTCTTGGAGCAG 602  
DB 364 GCGCTGCGCTTCAACCGCTTCAAGCTGTCATCATGAAGTTCTTGGAGCAG 423

QY 603 ATCTTCAAGAACAGCTTGAACCAACCTGCTCCATGAGGCGGCGCAAGGCGGCTCCGACTTC 662  
DB 424 ATCTTCAAGAACAGCTTGAACCAACCTGCTCCATGAGGCGGCGCAAGGCGGCTCCGACTTC 483  
QY 663 GACCCCAAGGCGCAAGAGAGCGCGAGGTGATGCGCTTCTCCAGTCTCTTCAATGACCGAG 722  
DB 484 GACCCCAAGGCGCAAGAGAGCGCGAGGTGATGCGCTTCTCCAGTCTCTTCAATGACCGAG 543  
QY 723 CTGCAAGCGCAATCAAGCTACGTGACAGAGCGTCCCGCGGCGCAATGCGGTGAGCGCG 782  
DB 544 CTGCAAGCGCAATCAAGCTACGTGACAGAGCGTCCCGCGGCGCAATGCGGTGAGCGCG 603  
QY 783 GCGGAGATGCTGACCTTTTCCGCGAGTACAGAGCGATCAACAGAACTAAGCCGCGTG 842  
DB 604 GCGGAGATGCTGACCTTTTCCGCGAGTACAGAGCGATCAACAGAACTAAGCCGCGTG 663  
QY 843 CTGACCCCGAAGGCGCAGAGATATGCGGCTCCAGATCCGCGCGAGCGCACCGGCTAC 902  
DB 664 CTGACCCCGAAGGCGCAGAGATATGCGGCTCCAGATCCGCGCGAGCGCACCGGCTAC 723  
QY 903 GCGCGCTGCTGTTTGTGAGAACGTGCTGAAGAACAGGCGAGAGCTTCAAGGCGCAG 962  
DB 724 GCGCGCTGCTGTTTGTGAGAACGTGCTGAAGAACAGGCGAGAGCTTCAAGGCGCAG 783  
QY 963 GCGTGCCTGCTGCTGCGCGCGCGGCAAGTGGCCAGTACTGCGGAGCTGCTGAG 1022  
DB 784 GCGTGCCTGCTGCTGCGCGCGGCAAGTGGCCAGTACTGCGGAGCTGCTGAG 843  
QY 1023 AAGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1082  
DB 844 AAGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903  
QY 1083 TTCAAGCGCGCAGCAGCTGCGAGCGGTGCAAGACATGAAGAAAGAACAGCGCGCGC 1142  
DB 904 TTCAAGCGCGCAGCAGCTGCGAGCGGTGCAAGACATGAAGAAAGAACAGCGCGCGC 963  
QY 1143 ATCTCCAGATCAAGAGCGACCGCGGTGATGTCGCGCGCAAGCGCGCTTGGAG 1202  
DB 964 ATCTCCAGATCAAGAGCGACCGCGGTGATGTCGCGCGCAAGCGCGCTTGGAG 1023  
QY 1203 CTGAGTGCAGGAGTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1262  
DB 1024 CTGAGTGCAGGAGTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1083  
QY 1263 GACGCGGAGCTGCTGATCAAGCAGCGCTGCGAGTACGTGTCGAGGCGCGCAATGCGCC 1322  
DB 1084 GACGCGGAGCTGCTGATCAAGCAGCGCTGCGAGTACGTGTCGAGGCGCGCAATGCGCC 1143  
QY 1323 TCCACCAAGAGCGCATTCACAGTACACAGGCGCGCATCATCTACTGCTCCGCGCAG 1382  
DB 1144 TCCACCAAGAGCGCATTCACAGTACACAGGCGCGCATCATCTACTGCTCCGCGCAG 1203  
QY 1383 GCGGCGCAACCGCGCGCGGTGCGGTGAGCGGCTGAGAGTGAACCGCAACCGCATGAGC 1442  
DB 1204 GCGGCGCAACCGCGCGCGGTGCGGTGAGCGGCTGAGAGTGAACCGCAACCGCATGAGC 1263  
QY 1443 CTGAAGTGAACCTCGCGAGAGGTTCGAGCAACGCTGAGCGCATCATGAAGAGCATCTAC 1502  
DB 1264 CTGAAGTGAACCTCGCGAGAGGTTCGAGCAACGCTGAGCGCATCATGAAGAGCATCTAC 1323  
QY 1503 GACTCCGCGATGCGGCGGTTCGCGAGATACATCTTGAATCTGCTGCGGCGCGCAATC 1562  
DB 1324 GACTCCGCGATGCGGCGGTTCGCGAGATACATCTTGAATCTGCTGCGGCGCGCAATC 1383  
QY 1563 GCGGCGCTTCAACAGGAGTGAATGCGGTCAAGGCGCGAGGCGCTGTTTAAGCTGCGCAG 1622  
DB 1384 GCGGCGCTTCAACAGGAGTGAATGCGGTCAAGGCGCGAGGCGCTGTTTAAGCTGCGCAG 1443  
QY 1623 GCGGCGCGACGCGCTCAACCGGCAATCCAC 1652  
DB 1444 GCGGCGCGACGCGCTCAACCGGCAATCCAC 1473

RESULT 14  
US-08-828-451-25  
Sequence 25, Application US/08828451  
Patent No. 5985634  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBSTITUTED OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Saliwanhik & Saliwanhik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,451  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1473 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 4..1431  
US-08-828-451-25

Query Match 68.7%; Score 1470; DB 2; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 4.1e-289;  
Matches 1470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 ATGACGCGCACCGGCGGACTTCAACGCGCTGCGAGAGGCGGTGAAGCAGATGCGCAC 242  
DB 4 ATGACGCGCACCGGCGGACTTCAACGCGCTGCGAGAGGCGGTGAAGCAGATGCGCAC 63  
QY 243 AAGGCGGCGACTGAGGCGCTGTGTCACGCGCATCAAGAACCCCGAGTGGCGGAGCTGTG 302  
DB 64 AAGGCGGCGACTGAGGCGCTGTGTCACGCGCATCAAGAACCCCGAGTGGCGGAGCTGTG 123  
QY 303 ACCGAGATCTTCATGAAGAACCCCGAGGAGGAGTTCATGCGGCGGTGGGAGGTTG 362  
DB 124 ACCGAGATCTTCATGAAGAACCCCGAGGAGGAGTTCATGCGGCGGTGGGAGGTTG 183  
QY 363 GCGGCTCCCTGCGAGCCCGTGTTCGAGAGGCGCCCGAGTGTGCGCCATCTTCAAGCAG 422  
DB 184 GCGGCTCCCTGCGAGCCCGTGTTCGAGAGGCGCCCGAGTGTGCGCCATCTTCAAGCAG 243  
QY 423 ATCTGTGAGCTGAGGCGGTGATCACTTCCGCGGTCTCTGCTGAGAGCAGCGCGGCAAC 482  
DB 244 ATCTGTGAGCTGAGGCGGTGATCACTTCCGCGGTCTCTGCTGAGAGCAGCGCGGCAAC 303

QY 483 CTGCAAGGTCAACCGCGGCTTCCGCGTGCAGTACTGTCGCGCATCGGCCCTTCAAGGCG 542  
DB 304 CTGCAAGGTCAACCGCGGCTTCCGCGTGCAGTACTGTCGCGCATCGGCCCTTCAAGGCG 363  
QY 543 GCGCTGCGCTTCAACCCCTCCGTGAACCTGTGCATCATGAAGTTCTTCTGCTTTGAGCAG 602  
DB 364 GCGCTGCGCTTCAACCCCTCCGTGAACCTGTGCATCATGAAGTTCTTCTGCTTTGAGCAG 423  
QY 603 ATCTTCAAGAACAGCTGACCACTTCCGCGGTGAGGCGGCGGCAAGGCGGCTCCGACTTC 662  
DB 424 ATCTTCAAGAACAGCTGACCACTTCCGCGGTGAGGCGGCGGCAAGGCGGCTCCGACTTC 483  
QY 663 GACCCCAAGGGCAAGAGCGAGCGGAGGTATCGCTTTCGCAAGTCTTCAATGACCGAG 722  
DB 484 GACCCCAAGGGCAAGAGCGAGCGGAGGTATCGCTTTCGCAAGTCTTCAATGACCGAG 543  
QY 723 CTGCAAGCGCAATCACTACGTGCAAGAGCTGTCCCGCGGCGCAATCGCGTGGGCGG 782  
DB 544 CTGCAAGCGCAATCACTACGTGCAAGAGCTGTCCCGCGGCGCAATCGCGTGGGCGG 603  
QY 783 CGGAGATTGGCTTACCTTTCCGCGAGTACCAAGGATCAACGAACTACCGGCGTG 842  
DB 604 CGGAGATTGGCTTACCTTTCCGCGAGTACCAAGGATCAACGAACTACCGGCGTG 663  
QY 843 CTGACCCCGAAGGGCGAGAGTATGGCGGCTCCGAGATCCCGCGGCGCAACCGGCTAC 902  
DB 664 CTGACCCCGAAGGGCGAGAGTATGGCGGCTCCGAGATCCCGCGGCGCAACCGGCTAC 723  
QY 903 GCGCGCTGTCTTGTGTGAGAACGTGTGAAGAGCAAGGCGGAGCTCAAGGCGCAG 962  
DB 724 GCGCGCTGTCTTGTGTGAGAACGTGTGAAGAGCAAGGCGGAGCTCAAGGCGCAG 783  
QY 963 CGCTGCTGTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1022  
DB 784 CGCTGCTGTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 843  
QY 1023 AAGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1082  
DB 844 AAGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903  
QY 1083 TTCAAGGCGGAGCAGCTGAGGCGGTGCGAGAGATGAAGAAAGAACCAAGCGCGCGC 1142  
DB 904 TTCAAGGCGGAGCAGCTGAGGCGGTGCGAGAGATGAAGAAAGAACCAAGCGCGCGC 963  
QY 1143 ATCTCCAGTACCAAGAGCGCACCGCGGTATGTGGCGGCGGCGGCGGCGGCGGCGGCGG 1202  
DB 964 ATCTCCAGTACCAAGAGCGCACCGCGGTATGTGGCGGCGGCGGCGGCGGCGGCGGCGG 1023  
QY 1203 CTGGAATGCGAGGTGAGCATGCGCTTCCCTGCGCGCACCGAGAACGATCGATGAGCAC 1262  
DB 1024 CTGGAATGCGAGGTGAGCATGCGCTTCCCTGCGCGCACCGAGAACGATCGATGAGCAC 1083  
QY 1263 GACGCGAGTGTGTATCAAGCAAGGCTGCAAGTGTGTGAAGGCGCGCAATGCCCC 1322  
DB 1084 GACGCGAGTGTGTATCAAGCAAGGCTGCAAGTGTGTGAAGGCGCGCAATGCCCC 1143  
QY 1323 TTCAAGCAAGAGCGCATCCCAAGTACCAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1382  
DB 1144 TTCAAGCAAGAGCGCATCCCAAGTACCAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1203  
QY 1383 GCGGCGCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1442  
DB 1204 GCGGCGCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1263  
QY 1443 CTGAATGGAATGCGAGAGGTTTCGGAACAAGCTGAGAGCGCATGTGAAGACATTTAC 1502  
DB 1264 CTGAATGGAATGCGAGAGGTTTCGGAACAAGCTGAGAGCGCATGTGAAGACATTTAC 1323  
QY 1503 GACTCGGCGCATGGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1562  
DB 1324 GACTCGGCGCATGGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1383

Qy 1563 GCGGCTTACCAAGGCTGATGCTCAAGGCGGCGCTTTAAGCTGCCAG 1622  
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Qy 1623 GCCCAAGCAGGCTCACCAGCATCCAAAC 1652  
Db 1444 GCCCAAGCAGGCTCACCAGCATCCAAAC 1473

## RESULT 15

US-09-252-991A-4131/c  
; Sequence 4131, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 4131  
; LENGTH: 1497  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-4131

Query March 27.7%; Score 592.2; DB 4; Length 1497;

Best Local Similarity 68.1%; Pred. No. 6.1e-111; Matches 889; Conservative 0; Mismatches 398; Indels 18; Gaps 4;

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Qy 381 GTGTTCGAGAACCGCCGAGCTGCTG-----CCCATCTTCAAGCAGATGTTAGCCT 434  
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Qy 435 GAGGCGGTGATCATTCCCGGTGCTGCTGATGCAAGCGCGGCAACTGAGTCAAC 494  
Db 1305 GAGGCGGTGATCATTCCCGGTGCTGCTGATGCAAGCGCGGCAACTGAGTCAAC 1246  
Qy 495 GCGGCTTCCGCTGAGTACTGTCGCGCATCGGCCCTCAAGAGGCGGCTGCGCTTC 554  
Db 1245 GTGGCTACCGGGGTGAGATGAGCAGCGCCATCGGCCCTCAAGAGGCGGCTGCGCTTC 1186  
Qy 555 CACCCCTCCGTGAACCTGTCATCATGAACTTCCTTGGCTTTGAGCAGATCTTCAAGAAC 614  
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Db 1125 TCCCTGACCACTGCTCCCATGAGGCGGCGCAAGGCGGCTTCGACTTGAACCCCAAGGCG 1066  
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Db 885 GGCTGAGTATGAGCGGCGAGCTGATCCGCCGAGAGCGACCGGCTTCCGCTGCGTCTAC 826  
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Db 825 TTGCGCCAGGAATGCTCAAGAGATGTCGCGCGCTTCAGCGGCGAGCGGCTGCTGCTG 766  
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Qy 1095 CAGCTGAGGCGGCTGAGAGATTAAGAAAGAAACAAAGCGGCGGCTTCCGAGTAC 1154  
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Qy 1215 GTGACATCGCTTCCTTCGAGCTTCTGAAAGGCGCGGCTTGGGCTGCTGCTG--- 1274  
Db 531 ---GATATCGGCTGCTGCTGCGGAGCCAGAGAGTGTGCGAGATGCGCGGCGC 475  
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Job time : 388 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2005, 19:09:08 ; Search time 1204 Seconds  
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Title: US-10-627-886-1

Perfect score: 2140

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Scoring table: IDENTITY NUC

Gap: 10.0, Gapext 1.0

Searched: 6330943 seqs, 3139157217 residues

Total number of hits satisfying chosen parameters: 1266186

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications NA:\*

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- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
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- 25: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2140	100.0	2140	9	US-10-627-886-1
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4	2137	99.9	2137	19	US-10-627-886-18
5	2046	95.6	2099	9	US-09-070-844-3
6	2046	95.6	2099	19	US-10-627-886-3
7	2043	95.5	2096	9	US-09-070-844-19

8	2043	95.5	2096	19	US-10-627-886-19	Sequence 19, Appl
9	1969	92.0	1969	9	US-09-070-844-7	Sequence 7, Appl
10	1969	92.0	1969	9	US-10-627-886-7	Sequence 23, Appl
11	1501.4	70.2	1506	9	US-09-070-844-23	Sequence 23, Appl
12	1501.4	70.2	1506	19	US-10-627-886-23	Sequence 23, Appl
13	1470	68.7	1473	9	US-09-070-844-25	Sequence 25, Appl
14	1470	68.7	1473	19	US-10-627-886-25	Sequence 25, Appl
15	590.8	27.6	1338	17	US-10-282-122A-30503	Sequence 30503, A
16	572.4	26.7	2256646	19	US-10-470-566-1	Sequence 1, Appl
17	529.2	24.7	1392	17	US-10-282-122A-15094	Sequence 15094, A
18	526.2	24.6	1347	17	US-10-282-122A-31354	Sequence 31354, A
19	508.2	23.7	1275	17	US-10-369-493-24304	Sequence 24304, A
20	500.4	23.4	1314	17	US-10-369-493-34308	Sequence 34308, A
21	489.8	23.4	1335	17	US-10-369-493-37634	Sequence 37634, A
22	488.6	22.8	1332	17	US-10-282-122A-28945	Sequence 28945, A
23	472.6	22.1	1332	18	US-10-282-122A-151	Sequence 151, App
24	472.6	22.1	1335	17	US-10-282-122A-29857	Sequence 29857, A
25	460.8	21.5	1344	17	US-10-369-493-31902	Sequence 31902, A
26	448.6	21.0	1524	18	US-10-425-114-13968	Sequence 13968, A
27	447	20.9	1341	17	US-10-282-122A-24059	Sequence 24059, A
28	435.8	20.4	3309400	9	US-09-738-626-1	Sequence 1, Appl
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31	422.6	19.7	1108	17	US-10-369-493-32481	Sequence 32481, A
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34	409.6	19.1	1341	17	US-10-282-122A-36585	Sequence 36585, A
35	396	18.5	1362	17	US-10-369-493-33526	Sequence 33526, A
36	389.8	18.2	1344	17	US-10-369-493-24546	Sequence 24546, A
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38	374.6	17.5	1344	17	US-10-282-122A-17814	Sequence 17814, A
39	358.4	16.7	1332	17	US-10-282-122A-12258	Sequence 12258, A
40	342.8	16.0	1347	17	US-10-282-122A-37840	Sequence 37840, A
41	341	15.9	12666	8	US-08-961-527-137	Sequence 137, App
42	341	15.9	12666	17	US-10-158-844-137	Sequence 137, App
43	340.4	15.9	2162598	21	US-10-472-928-49579	Sequence 49579, A
44	338.2	15.8	1341	17	US-10-369-493-44956	Sequence 44956, A
45	337.4	15.8	1344	17	US-10-282-122A-42104	Sequence 42104, A

#### ALIGNMENTS

RESULT 1  
US-09-070-844-1  
Sequence 1, Application US/09070844  
Patent No. US20020062495A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070, 844  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,596  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2140 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 33..1610  
US-09-070-844-1

Query Match 100.0%; Score 2140; DB 9; Length 2140;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2101 GTAAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140

RESULT 2
US-10-627-886-1
; Sequence 1, Application US/10627886
; Publication No. US20040128710A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
MILLER, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION/ON: 33..1610

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[illegible]



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QY 304 CCGAGATTTTCAATGAAAGACCCCGAGACAGCAAGATTCAATGCAAGCGGTGGCGAGGTGG 363  
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QY 364 CCGCTCCCTGAGCGCCGTTGTTGAGAGCGCCCGAAGCTGCTGCTTCAATTTCAAGCAGA 423  
Db 361 CCGTCTCCCTGAGCGCCGTTGTTGAGAGCGCCCGAAGCTGCTGCTTCAATTTCAAGCAGA 420  
QY 424 TCGTTGAGCCTGAGCGCGTGAATCACTTCCGCGTGTCTGCTGAGACAGCGCGCAACC 483  
Db 421 TCGTTGAGCCTGAGCGCGTGAATCACTTCCGCGTGTCTGCTGAGACAGCGCGCAACC 480  
QY 484 TGCAGTCAACCGCGGCTTCCGCGTGAATCACTGCTGCGCAATGCGCCCTTCAAGAGGCG 543  
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QY 544 GCGTGGCTTCAACCCCTCCGTTGAACCTGTCATGTAAGTTCTTGCCTTTGAGCAGA 603  
Db 541 GCGTGGCTTCAACCCCTCCGTTGAACCTGTCATGTAAGTTCTTGCCTTTGAGCAGA 600  
QY 604 TCTTCAAGAACAGCCTGACCAACCTGCGCATGAGCGCGCAAGGCGGCTCCGACTTGG 663  
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Db 1261 AGCGGAGCTGTGATCAAGCAAGCGCTGCAGATAGTGTGAGGCGCCCAATGCTCT 1320  
QY 1324 CCACCAAGAGGCGCATCAAGATACAAAGAGGCGGAGATCATCTACGCGCGGCAAG 1383

Db 1321 CCACCAAGAGGCGCATCAAGATACAAAGAGGCGGAGATCATCTACGCGCGGCAAG 1380  
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Db 1381 CCGCCAAAGCGCGGCGGTGGCGGTGACCGGCTTGAAGATTAACCAAGAACCGCATGAGCC 1440  
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Db 1441 TGAAGTGCAGAGTGAATGCGCTTCCCTGCGCCAGCCAGATGATGAGAGCAATCTTACG 1500  
QY 1504 ACTCGGCATAGGGCGGTGCGCGAGATACATGTTGACTGCTGCGCGCGCAACATG 1563  
Db 1501 ACTCGGCATAGGGCGGTGCGCGAGATACATGTTGACTGCTGCGCGCGCAACATG 1560  
QY 1564 CCGGCTTCAACCAAGTGTGATGCGCTCAAGGCGCGAGGCGCTGTTTAACTGCGCAAG 1623  
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QY 1864 GAGCTCGCGCGAATTTGCTGCGACATGCTGCTGTTTGAAGCCCTTCAAGTCAACCA 1923  
Db 1861 GAGCTCGCGCGAATTTGCTGCGACATGCTGCTGTTTGAAGCCCTTCAAGTCAACCA 1920  
QY 1924 CTGTTTGAAGCTTACAGCTCAATGCTTTTGAATGATGAGCGCCCTCTGCGCC 1983  
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QY 1984 CGAATTTTCTGCGCATAGAGAGTGGCTTCTTACCTGAGTGAACCCCAAGTGAAGT 2043  
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QY 2044 GTGCGTCTTGCCTGCGCTGCGCGGAGTGCATCTGTGACTGAGAGTGTGTGTA 2103  
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Db 2101 AACACGACGAGTCAAAAAAAAAAAAAAAAAAAAA 2137

RESULT 4  
US-10-627-886-18  
; Sequence 18, Application US/10627886  
; Publication No. US20040128710A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE  
; DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanichik & Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606-6669



Db	1631	CCCAAGCACAAGCTCACCGGATTCMAACCAACCACTCAACGGCCAGAGCTTTTGG	1688
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Qy	1744	GCCTGCCCCCTGCATTTCACCCCAAGAAAGAACTGAGGGGCACTTGATCAGAGCG	1803
Db	1741	GCCGTGCCCCCTGCATTTCACCCCAAGAAAGAACTGAGGGGCACTTGATCAGAGAGG	1800
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Qy	1864	GACGTCGCGCCGACTTTTGCGACATGCTCGGTTTGAACCCCTTCAGTTCACCCAC	1923
Db	1861	GACGTCGCGCCGACTTTTGCGACATGCTCGGTTTGAACCCCTTCAGTTCACCCAC	1920
Qy	1924	CCTGTGTGAAGCCCAACAGCTCAATTGGCTTTAAGTATGTGGCCCCCTCTCGCCCC	1983
Db	1921	CCTGTGTGAAGCCCAACAGCTCAATTGGCTTTAAGTATGTGGCCCCCTCTCGCCCC	1980
Qy	1984	CGAATTTTCCTGCATGAGAGCTGCGGTTCTTCAAGCTGTGACCCCAAGTAGACATTAGT	2043
Db	1981	CGAATTTTCCTGCATGAGAGCTGCGGTTCTTCAAGCTGTGACCCCAAGTAGACATTAGT	2040
Qy	2044	GTCGTGCTTTGCCCCCTGCGCTGCCGGGATGCGATATCTGTGACCTGAGAGTGTGTGTA	2103
Db	2041	GTCGTGCTTTGCCCCCTGCGCTGCCGGGATGCGATATCTGTGACCTGAGAGTGTGTGTA	2100
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Db	2101	AACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2137	

RESULT 5  
 US-09-070-844-3  
 ; Sequence 3, Application US/09070844  
 ; Patent No. US20020062495A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmidt, Robert R.  
 ; APPLICANT: Miller, Philip  
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
 ; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
 ; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/070,844  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/725,596  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Whitlock, Ted W.  
 ; REGISTRATION NUMBER: 36,965  
 ; REFERENCE/DOCKET NUMBER: UP155  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (904) 375-8100  
 ; TELEFAX: (904) 372-5800

```

; INFORMATION FOR SEQ ID NO: 3:
;
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 2099 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
;
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: 33..1568
;
US-09-070-844-3

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Query Match	95.6%	Score 2046	DB 9	Length 2099
Best Local Similarity	98.0%	Pred. No. 0		
Matches 2098	Conservative	0	Mismatches	0
			Indels	42
			Gaps	1
Qy	1	CTCCCTTCTGCTCCGCCCTCTCTCCGTCCCGCATGACAGCCGCTCGTCCCAAGCTTA	60	
Dp	1	CTCTTTTCTGCTCCGCCCTCTCTCCGTCCCGCATGACAGCCGCTCGTCCCAAGCTTA	60	
Qy	61	TCGTGGCCCGCCCGCTGAGCGGACGCCCCGCGTGCCTCGCGCGTGGCCGTGGCG	120	
Dp	61	TCGTGGCC-----TGCGCGTGGG	78	
Qy	121	TCGCCTCCGCCAAGCGGATGTCCGCGCCCAAGGCGCTCTCGCTGAGAGAGATCTCCG	180	
Dp	79	TCGCCTCCGCCAAGCGGATGTCCGCGCCCAAGGCGCTCTCGCTGAGAGAGATCTCCG	138	
Qy	181	CGATGAGACGCCACACCGCGCATTTCAACGCGCTGACAGAAAGCGGTGAAAGATGAGCA	240	
Dp	139	CGATGAGACGCCACACCGCGCATTTCAACGCGCTGACAGAAAGCGGTGAAAGATGAGCA	198	
Qy	241	CCAAGGCGGCGCATGAGGGCTGTGTGACCGGCATCAAGAACCCCGACGTGGCGCAGCTGC	300	
Dp	199	CCAAGGCGGCGCATGAGGGCTGTGTGACCGGCATCAAGAACCCCGACGTGGCGCAGCTGC	258	
Qy	301	TGACCGAGATCTTATGAGAGACCCGAGACAGCAGAGATTATATCAGCGGTGGCGGAG	360	
Dp	259	TGACCGAGATCTTATGAGAGACCCGAGACAGCAGAGATTATATCAGCGGTGGCGGAG	318	
Qy	361	TGGCGGATCTCCGTGACACCGCGTGTGTGAGAAAGCGCCCGAGCTGCTGCCATCTTCAAG	420	
Dp	319	TGGCGGATCTCCGTGACACCGCGTGTGTGAGAAAGCGCCCGAGCTGCTGCCATCTTCAAG	378	
Qy	421	AGATCGTTGAGCTGACGCGGTGATCACTTCCGCGTGTCTGTGACGACGCGCGCA	480	
Dp	379	AGATCGTTGAGCTGACGCGGTGATCACTTCCGCGTGTCTGTGACGACGCGCGCA	438	
Qy	481	ACCTGCAGGTCAACCGCGGCTTCCGCGTGACGATCTGTCCGCGCATGGCCCTTACAGG	540	
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Qy	601	AGATCTTCAAGAACAGCGCTGACCACTCTGCCATAGGCGCGGCAAGGCGGCTCCGACT	660	
Dp	559	AGATCTTCAAGAACAGCGCTGACCACTCTGCCATAGGCGCGGCAAGGCGGCTCCGACT	618	
Qy	661	TCGACCCCAAGGCGAAGGCGACGCGGAGGTGATGTCGCTTCTGGCACTCTTACGACG	720	
Dp	619	TCGACCCCAAGGCGAAGGCGACGCGGAGGTGATGTCGCTTCTGGCACTCTTACGACG	678	
Qy	721	AGCTGCAGCGCCACATGATGATGATGAGACGTGCCCCGCGGTGACATATGGGCGTGGGCG	780	
Dp	679	AGCTGCAGCGCCACATGATGATGATGAGACGTGCCCCGCGGTGACATATGGGCGTGGGCG	738	
Qy	781	CGCGCGAGATTGGCTACTTTTGGCCAGTACAAAGCGCATCAACAAGATTACACCGGCG	840	
Dp	739	CGCGCGAGATTGGCTACTTTTGGCCAGTACAAAGCGCATCAACAAGATTACACCGGCG	798	
Qy	841	TGCTGACCCCGAAGGCGCAGAGATGTCGCGCTTCGAGATCGGCCCGGAGGCCACGCGT	900	





Qy 1 CTCCTTTCGTGCTGCTCTCTCTCGTCCGCGCCATGCAAGCACCGCTCTGTCGCAAGCTTA 60  
Db 1 CTCCTTTCGTGCTGCTCTCTCTCGTCCGCGCCATGCAAGCACCGCTCTGTCGCAAGCTTA 60  
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Db 61 TGTGTGCGCGCGCGCTGTGCGGCAAGCCGCGCTGCTGTGCGCGCTGTGCGCGCTGTGCG 120  
Qy 121 TCCGCTTCGCGCAAGGCGCGATGTGCGCGCGCGCGCGCTGTGCGCGCGCGCGCGCGCG 180  
Db 79 TCCGCTTCGCGCAAGGCGCGATGTGCGCGCGCGCGCGCTGTGCGCGCGCGCGCGCGCG 138  
Qy 181 CGATGGAAGCGCAACACCGCGCGCTTCAAGCGCTGTGCAAGAGCGCGTGAAGCATGAGCA 240  
Db 139 CGATGGAAGCGCAACACCGCGCGCTTCAAGCGCGCTGTGCAAGAGCGCGTGAAGCATGAGCA 198  
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Qy 421 AGATGTTGAGCTTGAAGCGCGCTGATCACTTCCGCGTGTCTGCGTGAAGCAAGCGCGCA 480  
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Qy 481 ACCTGAGAGTCAACCGCGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
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Db 979 AGAAGGCGCGCATGCTGT 1038  
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Qy 1441 GCTGAACTGGAATCGGAGAGGCTTCCGCGAGTGAAGCGCGCGCGCGCGCGCGCGCG 1500  
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Qy 1741 GCG 1800  
Db 1699 GCG 1758  
Qy 1801 CGGCTATTTTTCGCGAGCGCGCTCACCGCGAGCGCTCTCCCGCGAGCGCTTAAGC 1860  
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Qy 1861 GCTGAGCTGCG 1920  
Db 1819 GCTGAGCTGCG 1878  
Qy 1921 CACCTGTGTGGAAGCTTACAGCTCAATTGCTTTTGTGTGTGTGTGTGTGTGTGTGT 1980  
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Qy 1981 CCGCGAATTTTTCGCGCATGAGAGCGTGTGCTTACCTGTGTGTGTGTGTGTGTGTGT 2040  
Db 1939 CCGCGAATTTTTCGCGCATGAGAGCGTGTGCTTACCTGTGTGTGTGTGTGTGTGTGT 1998  
Qy 2041 AGTGTGCGT 2100  
Db 1999 AGTGTGCGT 2058  
Qy 2101 GTTAAACGAGAGCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2140  
Db 2059 GTTAAACGAGAGCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098

RESULT 7

US-09-070-844-19  
Sequence 19, Application US/09070844  
Patent No. US20020062495A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,844  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,596  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whillock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2096 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-070-844-19

Query Match 95.5%; Score 2043; DB 9; Length 2096;  
Best Local Similarity 98.0%; Pred. No. 0;  
Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

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QY 64 TGGCCGCCCCCGCTGGCGGACGCCCGCGCTGCGCCCTGCGCCGCTGCGCGTGC 123  
DB 61 TGGCC-----TGCCCGTGGGTCC 78  
QY 124 GCTCCGCGCAGCGGATGTCGCGCGCAAGCGCGTCTGCTGGAGAGAGATCTCCGCGA 183  
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DB 139 TGGAGCGCACCGACCGGCACTTCAACGCGCTGCAAGAGCGGCTGAAGAGAGATGCGACA 198  
QY 244 AGGCGGCGCATGAGGCGCTGTGTGCAACGCGCATCAAGAACCCGACGCTGGCGACGCTGTA 303  
DB 199 AGGCGGCGCATGAGGCGCTGTGTGCAACGCGCATCAAGAACCCGACGCTGGCGACGCTGTA 258  
QY 304 CCGAGATCTTGATGAAGAGACCGGAGACGAGAGATTCATGACGCGGCTGGCGAGAGTGG 363  
DB 259 CCGAGATCTTGATGAAGAGACCGGAGACGAGAGATTCATGACGCGGCTGGCGAGAGTGG 318

QY 364 CCGTCTCCCTGACGCCCGGTGTGAGAGCGCCCGAGCTGTGCCCATTTCAAGCAGA 423  
DB 319 CCGTCTCCCTGACGCCCGGTGTGAGAGCGCCCGAGCTGTGCCCATTTCAAGCAGA 378  
QY 424 TCGTTGAGCTGAGCGGCTATCACTTCCGCGTGTCTGCTGGAGAGAGCGCGCAACC 483  
DB 379 TCGTTGAGCTGAGCGGCTATCACTTCCGCGTGTCTGCTGGAGAGAGCGCGCAACC 438  
QY 484 TGAAGTCAACCGCGGCTTCCGCGTGCACTGCTCCGCGCATCGGCGCTTCAAGAGCG 543  
DB 439 TGAAGTCAACCGCGGCTTCCGCGTGCACTGCTCCGCGCATCGGCGCTTCAAGAGCG 498  
QY 544 GCTCGCGCTTCAACCCCTCCGTGAACCTGTCAATGAAGTTCTTGTGAGCAGA 603  
DB 499 GCTCGCGCTTCAACCCCTCCGTGAACCTGTCAATGAAGTTCTTGTGAGCAGA 558  
QY 604 TCTTCAAGAACAGCTTGAACCACTTGGCCATGGGCGCGGCAAGGGCGCTCCGACTTGG 663  
DB 559 TCTTCAAGAACAGCTTGAACCACTTGGCCATGGGCGCGGCAAGGGCGCTCCGACTTGG 618  
QY 664 ACCCGAAGGCGAAGAGCGAGCGGAGGTGATGCGCTTCTGCAATGATGACCGAGC 723  
DB 619 ACCCGAAGGCGAAGAGCGAGCGGAGGTGATGCGCTTCTGCAATGATGACCGAGC 678  
QY 724 TGCAGCGCACATCACTACGTACAGAGCGTCCCGCGCGCATTCGCGTGGCGCGC 783  
DB 679 TGCAGCGCACATCACTACGTACAGAGCGTCCCGCGCGCATTCGCGTGGCGCGC 728  
QY 784 GCGAGATTGGCTACTTTTGGCCAGTACAGAGGCAATCAAGAACTTACACCGCGCTGC 843  
DB 739 GCGAGATTGGCTACTTTTGGCCAGTACAGAGGCAATCAAGAACTTACACCGCGCTGC 798  
QY 844 TGAACCCGGAAGGCGAGAGATGAGCGGCTCCGAGATCCGCGCGGAGCGGCGCTACG 903  
DB 799 TGAACCCGGAAGGCGAGAGATGAGCGGCTCCGAGATCCGCGCGGAGCGGCGCTACG 858  
QY 904 GCGCGGTGCTGTTTGTGAGAGAACGTGCTGAAGGACAAAGGCGAGGCTTCAAGGCGAAGC 963  
DB 859 GCGCGGTGCTGTTTGTGAGAGAACGTGCTGAAGGACAAAGGCGAGGCTTCAAGGCGAAGC 918  
QY 964 GCTGCTGTGTCTGGCGCGGCGCAAGCGTGGCCAGTACGCGGCGAGCGTCTGTGAGA 1023  
DB 919 GCTGCTGTGTCTGGCGCGGCGCAAGCGTGGCCAGTACGCGGCGAGCGTCTGTGAGA 978  
QY 1024 AGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
DB 979 AGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038  
QY 1084 TCAACGCGAGACAGCTGCAAGCGGCTGCAAGCAATGAAGAAAGAAACACAGCGCGCGCA 1143  
DB 1039 TCAACGCGAGACAGCTGCAAGCGGCTGCAAGCAATGAAGAAAGAAACACAGCGCGCGCA 1098  
QY 1144 TCTCCGAGTACAAAGAGGACACCGCGCTGTATGTGGCGGACCGCGCAACCTTGGAGC 1203  
DB 1099 TCTCCGAGTACAAAGAGGACACCGCGCTGTATGTGGCGGACCGCGCAACCTTGGAGC 1158  
QY 1204 TGAAGTCCAGAGTGAATCATGCGCTTCCCTGCGCGCACCGAAGAGAGATGATGAGCAG 1263  
DB 1159 TGAAGTCCAGAGTGAATCATGCGCTTCCCTGCGCGCACCGAAGAGAGATGATGAGCAG 1218  
QY 1264 ACGCGAGCTGTGATCAAGACAGCGCTGCAAGTACGTGTGAGAGGCGCGCAATGCTT 1323  
DB 1219 ACGCGAGCTGTGATCAAGACAGCGCTGCAAGTACGTGTGAGAGGCGCGCAATGCTT 1278  
QY 1324 CCAACCAAGAGGCGCATCAAGTACAAAGGCGCGCATCACTTCTGCGCGGCAAGG 1383  
DB 1279 CCAACCAAGAGGCGCATCAAGTACAAAGGCGCGCATCACTTCTGCGCGGCAAGG 1338  
QY 1384 CCGGCAAGCGCGGCGGTGCGGCTCAAGCGGCTTGAAGATGACCCGAACCGGATGAGCC 1443  
DB 1339 CCGGCAAGCGCGGCGGTGCGGCTCAAGCGGCTTGAAGATGACCCGAACCGGATGAGCC 1398  
QY 1444 TGAAGTGAATTCGAGAGAGTTCGCGCAAGAGTGAAGCGCATCAAGAGACATTTACG 1503

Db 1399 TGAAGTGGAGTGGAGAGGTTGGCGAGCAAGCTGGAGCGCATGAGAGCAATCTACG 1458  
 Qy 1504 ACTCCCGCATATGGGCGCGTCCCGCAGATACATGTTGACCTGCGGGCGCCCAACATCG 1563  
 Db 1459 ACTCCCGCATATGGGCGCGTCCCGCAGATACATGTTGACCTGCGGGCGCCCAACATCG 1518  
 Qy 1564 CGGAGCTTCAACCAAGTGGCTATGATGCGGTCAAGGCGCAGGGGCGTGTAAAGTCCCGCAG 1623  
 Db 1519 CGGAGCTTCAACCAAGTGGCTATGATGCGGTCAAGGCGCAGGGGCGTGTAAAGTCCCGCAG 1578  
 Qy 1524 CCGAAGCCAGCGCTCACCGGCAATCCAAACCAACCACTCAACGCGCCAGACCTTTTCG 1683  
 Db 1579 CCGAAGCCAGCGCTCACCGGCAATCCAAACCAACCACTCAACGCGCCAGACCTTTTCG 1638  
 Qy 1684 AAGGCGGCGCTTTTCCAGCGAGGCGCTCACTGCGCTTTTCAATACCTGCTAATGGC 1743  
 Db 1639 AAGGCGGCGCTTTTCCAGCGAGGCGCTCACTGCGCTTTTCAATACCTGCTAATGGC 1698  
 Qy 1744 GCGGTGCGCCCTGCAATTCACCCCAAGAGAACTAGGCGCACTTGAAGTCAATCAAGACG 1803  
 Db 1699 GCGGTGCGCCCTGCAATTCACCCCAAGAGAACTAGGCGCACTTGAAGTCAATCAAGACG 1758  
 Qy 1804 CTATTTTTCGCGAGCGCGCTCAACCCGAGAGCTCTCCCGGAGCCCTAAGCGCT 1863  
 Db 1759 CTATTTTTCGCGAGCGCGCTCAACCCGAGAGCTCTCCCGGAGCCCTAAGCGCT 1818  
 Qy 1864 GAGCTCGCGCGCACTTGGCTCGACATCGCTGCGTGTGAAGGCGCTTCACTCAACCC 1923  
 Db 1819 GAGCTCGCGCGCACTTGGCTCGACATCGCTGCGTGTGAAGGCGCTTCACTCAACCC 1878  
 Qy 1924 CCGTGTGAAGGCTTACAGTCAATGCGCTTTTGAAGTATGATGCGCGCTTCTGCGCC 1983  
 Db 1879 CCGTGTGAAGGCTTACAGTCAATGCGCTTTTGAAGTATGATGCGCGCTTCTGCGCC 1938  
 Qy 1984 CGAATTTTCCTGATGAGAGTGGCTTCTAGCTGATGAGAGGCGGAGTGA 2043  
 Db 1939 CGAATTTTCCTGATGAGAGTGGCTTCTAGCTGATGAGAGGCGGAGTGA 1998  
 Qy 2044 GTGCGTGGCTTGGCTTGGCTGCGCGCGAGTGAATGTAAGTGAAGTGTGTGA 2103  
 Db 1999 GTGCGTGGCTTGGCTTGGCTGCGCGCGAGTGAATGTAAGTGAAGTGTGTGA 2058  
 Qy 2104 AACACGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140  
 Db 2059 AACACGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2095

RESULT 8  
 US-10-627-886-19  
 Sequence 19, Application US/10627886  
 Publication No. US20040128710A1  
 GENERAL INFORMATION:  
 APPLICANT: Schmidt, Robert R.  
 TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
 RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE  
 DEHYDROGENASES AND METHODS OF USE  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Saliwanchik & Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: Florida  
 COUNTRY: USA  
 ZIP: 32606-6669  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/627,886

FILING DATE: 24-Jul-2003  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/070,844  
 FILING DATE: 01-MAY-98  
 APPLICATION NUMBER: 08/725,596  
 FILING DATE: 03-OCT-96  
 APPLICATION NUMBER: 08/541,033  
 FILING DATE: 06-OCT-95  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lloyd, Jeff  
 REGISTRATION NUMBER: 35,589  
 REFERENCE/DOCKET NUMBER: UF-155C03  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (352) 375-8100  
 TELEFAX: (352) 372-5800  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2096 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
 US-10-627-886-19

Query Match 95.5%; Score 2043; DB 19; Length 2096;  
 Best Local Similarity 98.0%; Pred. No. 0;  
 Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

Qy 4 CTTTCGCTGCGCCCTCTCCGTCGCGGCAATGAGACCGGCGCTGTCGCAAGCTATCG 63  
 Db 1 CTTTCGCTGCGCCCTCTCCGTCGCGGCAATGAGACCGGCGCTGTCGCAAGCTATCG 60  
 Qy 64 TGGCGCGCGCGCTGCGGCAAGCGCGCTGCGCGGCGCTGCGCGGCGCTGCGCGGCTGCG 123  
 Db 61 TGGCGCGCGCGCTGCGGCAAGCGCGCTGCGCGGCGCTGCGCGGCGCTGCGCGGCTGCG 78  
 Qy 124 GCTCCGCAAGCGCGATGTCGCGGCAAGCGCGCTTCTGCTGAGAGACAGATCTCGCGA 183  
 Db 79 GCTCCGCAAGCGCGATGTCGCGGCAAGCGCGCTTCTGCTGAGAGACAGATCTCGCGA 138  
 Qy 184 TGAACGCAACACCGGCAATTCACGCGCGCTGAGAGAGGCGGTGAACATGCGCAACA 243  
 Db 139 TGAACGCAACACCGGCAATTCACGCGCGCTGAGAGAGGCGGTGAACATGCGCAACA 198  
 Qy 244 AGCGGCGCACTGAGAGGCGGTGTCACGCGCATCAAGAACCCGACGTGCGCAGTGTGA 303  
 Db 199 AGCGGCGCACTGAGAGGCGGTGTCACGCGCATCAAGAACCCGACGTGCGCAGTGTGA 258  
 Qy 304 CCGAGATCTTCATGAAGACCCGAGACGAGAGATTCATGCAAGCGGTGCGGAGTGG 363  
 Db 259 CCGAGATCTTCATGAAGACCCGAGACGAGAGATTCATGCAAGCGGTGCGGAGTGG 318  
 Qy 364 CCGTTCCTCTGACCGCGGTGTTGAGAGAGGCGCGGAGCTGCTGCCATTTCAAGAGA 423  
 Db 319 CCGTTCCTCTGACCGCGGTGTTGAGAGAGGCGCGGAGCTGCTGCCATTTCAAGAGA 378  
 Qy 424 TCGTTAGCGCTGAGCGGTGATCACTTCGCGCGTGTCTGCGGTGAGAGAGCGCGCAAC 483  
 Db 379 TCGTTAGCGCTGAGCGGTGATCACTTCGCGCGTGTCTGCGGTGAGAGAGCGCGCAAC 438  
 Qy 484 TGAAGTCAACCGCGCTTCGCGGTGAGAGAGTGTGTCGCGCATCGCGCTTCAAGAGCG 543  
 Db 439 TGAAGTCAACCGCGCTTCGCGGTGAGAGAGTGTGTCGCGCATCGCGCTTCAAGAGCG 498  
 Qy 544 GCTGCGCTTCAACCGCTTCGCGGTGAGAGAGTGTGTCGCGCATCGCGCTTCAAGAGCA 603  
 Db 499 GCTGCGCTTCAACCGCTTCGCGGTGAGAGAGTGTGTCGCGCATCGCGCTTCAAGAGCA 558  
 Qy 604 TCTTCAAGAACAGCTGACACCGCTGCGGTGAGAGAGGCGCGGAGCTTCAAGAGCTTGC 663  
 Db 559 TCTTCAAGAACAGCTGACACCGCTGCGGTGAGAGAGGCGCGGAGCTTCAAGAGCTTGC 618



US-09-070-844-7

Query Match 92.0%; Score 1969; DB 9; Length 1969;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

171 CAGATCTCCGCGATGAGCGCCACCGCGGACCTTCAAGCGGCTGACAGAGCGGCTGAG  
1 CAGATCTCCGCGATGAGCGCCACCGCGGACCTTCAAGCGGCTGACAGAGCGGCTGAG  
231 CAGATGCGCCACCAAGCGCGGCACTGAGGCGCTGTGTGACAGCGCATCAAGAGCCCGACGTC  
61 CAGATGCGCCACCAAGCGCGGCACTGAGGCGCTGTGTGACAGCGCATCAAGAGCCCGACGTC  
291 CCGCAGCTGTGACCGGAGATCTTCAATGAAGACCCGAGACAGAGAGATTCATGACGCG  
121 CCGCAGCTGTGACCGGAGATCTTCAATGAAGACCCGAGACAGAGAGATTCATGACGCG  
351 GTGCGGAGGTGCGCTCTCCCTGAGCGCGGTGTGAGAGCGCGCGGAGCTGTGCGC  
181 GTGCGGAGGTGCGCTCTCCCTGAGCGCGGTGTGAGAGCGCGCGGAGCTGTGCGC  
411 ATCTTCAAGCAGATGTTGAGCGCTGAGCGCGGTGATCACTTCCGCGTCTGTGAC  
241 ATCTTCAAGCAGATGTTGAGCGCTGAGCGCGGTGATCACTTCCGCGTCTGTGAC  
471 GAGCGCGGCACTGTGAGGTCAACCGCGGCTTCCGCGTGTGAGTACTGTCGCGCATCGGC  
301 GAGCGCGGCACTGTGAGGTCAACCGCGGCTTCCGCGTGTGAGTACTGTCGCGCATCGGC  
531 CCTTCAAGAGGCGGCTGCGGCTTCCAGCGCGTGTGAGAGCTGTGATGAGTACTGTC  
361 CCTTCAAGAGGCGGCTGCGGCTTCCAGCGCGTGTGAGAGCTGTGATGAGTACTGTC  
591 GCTTTGAGCAGATCTTCAAGAGCAGCTGACCACTGCGCATGAGCGCGGCAAGGCG  
421 GCTTTGAGCAGATCTTCAAGAGCAGCTGACCACTGCGCATGAGCGCGGCAAGGCG  
651 GCTTCCGATCTGAGCGCGGCAAGGCGCAGCGCGGAGGTGAGCGCTTGTGCGAGTCC  
481 GCTTCCGATCTGAGCGCGGCAAGGCGCAGCGCGGAGGTGAGCGCTTGTGCGAGTCC  
711 TTCAATGAGCAGATGTTGAGCGCTGAGCGCGGTGTGAGAGCGCGCGGAGTACTGTC  
541 TTCAATGAGCAGATGTTGAGCGCTGAGCGCGGTGTGAGAGCGCGCGGAGTACTGTC  
771 GCGGTGAGCGCGGCGGAGATGCTACTTTTCCGCGCAGTCAAGCGCATCAAGAGAC  
601 GCGGTGAGCGCGGCGGAGATGCTACTTTTCCGCGCAGTCAAGCGCATCAAGAGAC  
831 TACACCGGCGGTGAGCGCGGCAAGGCGCAGAGATGAGCGGCTCGAGATCCGCGCGAG  
661 TACACCGGCGGTGAGCGCGGCAAGGCGCAGAGATGAGCGGCTCGAGATCCGCGCGAG  
891 GCGCGGCGGTGAGCGCGGCGGTGTGAGAGCGGTGTGAGAGCGCGGAGTACTGTC  
721 GCGCGGCGGTGAGCGCGGCGGTGTGAGAGCGGTGTGAGAGCGCGGAGTACTGTC  
951 CTCAAGGCGCAAGCGCTGTGTGTGAGCGCGGCAAGTGTGAGTGTGAGTGTGAGTGTGAG  
781 CTCAAGGCGCAAGCGCTGTGTGTGAGCGCGGCAAGTGTGAGTGTGAGTGTGAGTGTGAG  
1011 CTGCTGTGAGAGAGGCGCGCATGTGTGTGAGCGCGGTGTGAGTGTGAGTGTGAGTGTGAG  
841 CTGCTGTGAGAGAGGCGCGCATGTGTGTGAGCGCGGTGTGAGTGTGAGTGTGAGTGTGAG  
1071 GAGCGCGGCGGTTCAGCGCGGAGCGTGTGAGCGCGGTGTGAGCGCGGTGTGAGTGTGAG  
901 GAGCGCGGCGGTTCAGCGCGGAGCGTGTGAGCGCGGTGTGAGCGCGGTGTGAGTGTGAG  
1131 AACAGCGCGCGCATCTCGAGTACAGAGCGACCGCGGTGTGAGTGTGAGTGTGAGTGTGAG  
961 AACAGCGCGCGCATCTCGAGTACAGAGCGACCGCGGTGTGAGTGTGAGTGTGAGTGTGAG

1191 AAGCTTTGGAGCTGAGACTGAGAGTGTGACATCGCTTCCCTGTGCGCCAGAGACGAG 1250  
1021 AAGCTTTGGAGCTGAGACTGAGAGTGTGACATCGCTTCCCTGTGCGCCAGAGACGAG 1080  
1251 ATCGATGAGCAGAGCGCGAGCTGTGATCAAGCAGGCTGCGAGTGTGAGAGGAG 1310  
1081 ATCGATGAGCAGAGCGCGAGCTGTGATCAAGCAGGCTGCGAGTGTGAGAGGAG 1140  
1311 GCGAATGCGCTTCCAGAGGCGCAGTCCAGAGTCAAGAGCGCGCATCTAC 1370  
1141 GCGAATGCGCTTCCAGAGGCGCAGTCCAGAGTCAAGAGCGCGCATCTAC 1200  
1371 TGCCCCGCGAGGCGCGCAGAGCGCGGCTGTGAGCGCGCTGTGAGAGTGTGAG 1430  
1201 TGCCCCGCGAGGCGCGCAGAGCGCGGCTGTGAGCGCGCTGTGAGAGTGTGAG 1260  
1431 AACCGATGAGCTGTGAGCTGCGAGAGAGGTGTGAGAGTGTGAGAGTGTGAG 1490  
1261 AACCGATGAGCTGTGAGCTGCGAGAGAGGTGTGAGAGTGTGAGAGTGTGAG 1320  
1491 AAGGATCTTACGACTCGCGCATGAGGCGGTCCGCGAGATCAATGTGTGACTGTG 1550  
1321 AAGGATCTTACGACTCGCGCATGAGGCGGTCCGCGAGATCAATGTGTGACTGTG 1380  
1551 GCGCGCAATCGCGGCGCTTACCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1610  
1381 GCGCGCAATCGCGGCGCTTACCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1440  
1611 TAAGTGTGCGAGGCGCGAGGCGGCTTACCGGAGTGTGAGTGTGAGTGTGAGTGTG 1670  
1441 TAAGTGTGCGAGGCGCGAGGCGGCTTACCGGAGTGTGAGTGTGAGTGTGAGTGTG 1500  
1671 AAGGATCTTGTGAGAGGCGCGCTTGTTCAGAGCGAGGCGCTTACCTGTGTGATTA 1730  
1501 AAGGATCTTGTGAGAGGCGCGCTTGTTCAGAGCGAGGCGCTTACCTGTGTGATTA 1560  
1731 CCTGTATTTGCGCGCGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1790  
1561 CCTGTATTTGCGCGCGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1620  
1791 TGATGAGAGAGGCTATTTTGTGCGAGCGGCGCTACCGCGAGAGCTGTCTCCCGG 1850  
1621 TGATGAGAGAGGCTATTTTGTGCGAGCGGCGCTACCGCGAGAGCTGTCTCCCGG 1680  
1851 AGCGCTTGTGAGAGGCGCGCTTGTTCAGAGCGAGGCGCTTACCTGTGTGATTA 1910  
1681 AGCGCTTGTGAGAGGCGCGCTTGTTCAGAGCGAGGCGCTTACCTGTGTGATTA 1740  
1911 CCACTTACCGAGCTGTGTGTGAGAGCTTACCGAGTGTGAGTGTGAGTGTGAGTGTG 1970  
1741 CCACTTACCGAGCTGTGTGTGAGAGCTTACCGAGTGTGAGTGTGAGTGTGAGTGTG 1800  
1971 CCGCTTGTGAGAGGCTTGTGTGAGAGCTTGTGTGAGAGGCTTGTGTGAGAGGCTTGT 2030  
1801 CCGCTTGTGAGAGGCTTGTGTGAGAGCTTGTGTGAGAGGCTTGTGTGAGAGGCTTGT 1860  
2031 AGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2090  
1861 AGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1920  
2091 GAGTGTGTGTGAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2139  
1921 GAGTGTGTGTGAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1969

RESULT 10

US-10-627-886-7

; Sequence 7, Application US/10627886

; Publication No. US20040128710A1

; GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606-6669

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/627,886  
FILING DATE: 24-Jul-2003  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/070,844  
FILING DATE: 01-MAY-98  
APPLICATION NUMBER: 08/725,596  
FILING DATE: 03-OCT-96  
APPLICATION NUMBER: 08/541,033  
FILING DATE: 06-OCT-95

ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: UF-155CD3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5880

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1969 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-627-886-7

Query Match 92.0%; Score 1969; DB 19; Length 1969;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

171 CAGATCTCCGCGATGACGCCACCAACCGGCGACTTTCACGCGCTGACAGAGCGGTAAG 230  
1 CAGATCTCCGCGATGACGCCACCAACCGGCGACTTTCACGCGCTGACAGAGCGGTAAG 60  
231 CAGATGCGCACCAAGCGCGGACATGAGGCGCTGTGTGACCGGCATCAAGAACCCGAGCTG 290  
61 CAGATGCGCACCAAGCGCGGACATGAGGCGCTGTGTGACCGGCATCAAGAACCCGAGCTG 120  
291 CGCAGAGCTGTGACCGGAGATCTTCATGAAGACCCGAGAGCAGAGAGTTGATGACGCG 350  
121 CGCAGAGCTGTGACCGGAGATCTTCATGAAGACCCGAGAGCAGAGAGTTGATGACGCG 180  
351 GTGCGCGAGGTGGCGCTCTCCCTGTGACGCGGTGTGGAAGAGCGCCCGAGCTGTGCGC 410  
181 GTGCGCGAGGTGGCGCTCTCCCTGTGACGCGGTGTGGAAGAGCGCCCGAGCTGTGCGC 240  
411 ATCTTCAAGAGATCTGTGAGCTGTGAGCGGTGATCACTTCCGCTGTCTGTGCTGAGC 470  
241 ATCTTCAAGAGATCTGTGAGCTGTGAGCGGTGATCACTTCCGCTGTCTGTGCTGAGC 300  
471 GAGCGCGGCAACTGTGAGAGTCAACCGGCGCTTCCGCGTGAAGTCTGTCCGCAATCGGC 530  
301 GAGCGCGGCAACTGTGAGAGTCAACCGGCGCTTCCGCGTGAAGTCTGTCCGCAATCGGC 360  
531 CCTTCAAGAGCGCGCTGTGAGTCAACCGGCGCTTCCGCGTGAAGTCTGTCCGCAATCGGC 590

361 CCTTACAGAGCGCGCTGCGCTTCCACCCCTCGTGAACCTGTGCAATCAAGAGTTCTT 420  
591 GCGTTAGAGAGATCTTCAAGAACAGCTGACACCCCTGCGCATTTGGCGCGCAAGGCG 650  
421 GCGTTAGAGAGATCTTCAAGAACAGCTGACACCCCTGCGCATTTGGCGCGCAAGGCG 480  
651 GCGTCCGACTTTCGACCCCAAGAGGCGAGAGCGAGGAGTGTGCGCTTCTGCACTCC 710  
481 GCGTCCGACTTTCGACCCCAAGAGGCGAGAGCGAGGAGTGTGCGCTTCTGCACTCC 540  
711 TTGATGACCGAGCTGTGACGCGCGCACATAGCTAGTGAAGAGTGTGCTGCGCGGAGATC 770  
541 TTGATGACCGAGCTGTGACGCGCGCACATAGCTAGTGAAGAGTGTGCTGCGCGGAGATC 600  
771 GCGCGGCGCGCGCGGAGTGTGCTGCTGCGCGGAGAGTGTGCGCGGAGAGTGTGCGCGG 830  
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831 TACACCGCGCTGTGACCGCGGAGAGGCGCAGAGATAGCGCGCTCCGAGATCCGCGCGAG 890  
661 TACACCGCGCTGTGACCGCGGAGAGGCGCAGAGATAGCGCGCTCCGAGATCCGCGCGAG 720  
891 GCGACCGGCTTACGCGCGCGCTGTGTTGTGAGAGAGTGTGAGAGAGAGAGGCGAGAGC 950  
721 GCGACCGGCTTACGCGCGCGCTGTGTTGTGAGAGAGTGTGAGAGAGAGAGGCGAGAGC 780  
951 CTCAAGGGCAAGAGCGCTGCTGTGTGCGCGCGGCAACGTTGCGCGCGAGTCTGCGCGGAG 1010  
781 CTCAAGGGCAAGAGCGCTGCTGTGTGCGCGCGGCAACGTTGCGCGCGAGTCTGCGCGGAG 840  
1011 CTGCTGTGAGAGAGGCGCGCATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1070  
841 CTGCTGTGAGAGAGGCGCGCATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 900  
1071 GAGGCCCAAGCGCTTACGCGCGGAGAGCTGTGAGCGGCTGTGAGAGAGAGAGAGAGAC 1130  
901 GAGGCCCAAGCGCTTACGCGCGGAGAGCTGTGAGCGGCTGTGAGAGAGAGAGAGAGAC 960  
1131 AACAGCGCGCGCGCATCTGCGAGTCAAGAGGAGCAACCGCGGTGTATGTGAGGCGAGC 1190  
961 AACAGCGCGCGCGCATCTGCGAGTCAAGAGGAGCAACCGCGGTGTATGTGAGGCGAGC 1020  
1191 AAGCTTGTGAGAGCTGTGACTGCGAGTGTGATGATGCTGCTGTGCTGTGCTGTGCTGTG 1250  
1021 AAGCTTGTGAGAGCTGTGACTGCGAGTGTGATGATGCTGCTGTGCTGTGCTGTGCTGTG 1080  
1251 ATGATGAGCAAGAGCGCGGAGCTGTGATCAAGAGCGGCTGTGAGTGTGAGAGGCG 1310  
1081 ATGATGAGCAAGAGCGCGGAGCTGTGATCAAGAGCGGCTGTGAGTGTGAGAGGCG 1140  
1311 GCCAACAATGCGCTTCAACCAAGAGGCGCATCAAGAGTCAAGAGGCGCGGATCATCTTAC 1370  
1141 GCCAACAATGCGCTTCAACCAAGAGGCGCATCAAGAGTCAAGAGGCGCGGATCATCTTAC 1200  
1371 TGCCCGGCAAGAGCGGCGCAACGCGCGGCGGTGTGAGCGGCTGTGAGATGAGCCAG 1430  
1201 TGCCCGGCAAGAGCGGCGCAACGCGCGGCGGTGTGAGCGGCTGTGAGATGAGCCAG 1260  
1431 AACCGCATGAGCTGTGAATGTGACTTCGCGAGAGAGTTTGGCAAGAGCTGTGAGCGCATATG 1490  
1261 AACCGCATGAGCTGTGAATGTGACTTCGCGAGAGAGTTTGGCAAGAGCTGTGAGCGCATATG 1320  
1491 AAGGACATCTACGACTCGGCGCATGAGGCGGTCCGCGAGATACATATGTTGACTGTGCGG 1550  
1321 AAGGACATCTACGACTCGGCGCATGAGGCGGTCCGCGAGATACATATGTTGACTGTGCGG 1380  
1551 GCGCGCAAACTCGCGGCTTACCAAGAGTGTGATGCTGTGAGAGCGGCGGCGCTGT 1610  
1381 GCGCGCAAACTCGCGGCTTACCAAGAGTGTGATGCTGTGAGAGCGGCGGCGGCTGT 1440  
1611 TAACTGCCCAAGCGCGCAAGCGGCTACCGGCAATCAACCGCAACTCAACGCGC 1670



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1506 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4..1464
; US-09-070-844-23

Query Match          70.2%; Score 1501.4; DB 9; Length 1506;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1502; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      150  AAGCCCGCTGCTGCGAGAGACATCTCCGCGATTGACCGGCACACCGCGGACTTCACG 209
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DB       4   ATGCGCGCTCTGCTGAGAGACCAATCTCCGCGATTGACCGGCACACCGCGGACTTCACG 63

QY      210  GCGCTGCAGAAAGGCGGTGAAGACAGATGGCCACCAAGGCGGCACTGAGGGCCTGGTGAC 269
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DB       64  GCGCTGCAGAAAGGCGGTGAAGACAGATGGCCACCAAGGCGGCACTGAGGGCCTGGTGAC 123

QY      270  GGCATCAAGAAACCCCGAGTGGCCGACGTGCTGACCCGAGATCTTCATGAAGAAGACCCGGAG 329
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DB       124  GGCATCAAGAAACCCCGAGTGGCCGACGTGCTGACCCGAGATCTTCATGAAGAAGACCCGGAG 183

QY      330  CAGCAGAGATTTCATGCACAGCGGTCGCGAGAGTGGCCGCTCTCCCTGCAGCCCGTGTTCAG 389
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DB       184  CAGCAGAGATTTCATGCACAGCGGTCGCGAGAGTGGCCGCTCTCCCTGCAGCCCGTGTTCAG 243

QY      390  AAGGCGCCCGGACCTGCTGCCATTCTTCAAGCAATCGTTAGCCTGAGCCGCTGATCAC 449
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OY	450	TTCCGCGGTCCTCTGGATCGAGAGCGCGGCAACTGGAGGCTCAACCGCGGCTTCCGCGTG	509
Db	304	TTCCGCGGTCCTCTGGATCGAGAGCGCGGCAACTGGAGGCTCAACCGCGGCTTCCGCGTG	363
OY	510	CAGTACTGTCGCGCATCGCGCCCTCAAGAGGCGGCTGCGCTTCAACCCCTCGTGAAC	569
Db	364	CAGTACTGTCGCGCATCGCGCCCTCAAGAGGCGGCTGCGCTTCAACCCCTCGTGAAC	423
OY	570	CTGTCCATCATGAAGTTCTTGCTTTGAGGAGATCTTCAAGAACAGCTTGAACCACTTG	629
Db	424	CTGTCCATCATGAAGTTCTTGCTTTGAGGAGATCTTCAAGAACAGCTTGAACCACTTG	483
OY	630	CCCAATGGGCGGCGGCAAGGCGGCTCCGACTTCACCCCAAGGGCAAGGCGAGCGGAG	689
Db	484	CCCAATGGGCGGCGGCAAGGCGGCTCCGACTTCACCCCAAGGGCAAGGCGAGCGGAG	543
OY	690	GTGATGCGCTTCTTCCAGTCTCTTCATGACCGAGCTGACGCGCAATCAGCTACGTGCG	749
Db	544	GTGATGCGCTTCTTCCAGTCTCTTCATGACCGAGCTGACGCGCAATCAGCTACGTGCG	603
OY	750	GACGTGCCCCCGGGCGCATTCGGGTGGGGCGCGCGGAGATTGGCTACTCTTTGGCGAG	809
Db	604	GACGTGCCCCCGGGCGCATTCGGGTGGGGCGCGCGGAGATTGGCTACTCTTTGGCGAG	663
OY	810	TACAGGCGCATCAACCAAGAACTACACCGGCGTGTGACCCCGAAGGGCCAGAGTATTGCG	869
Db	664	TACAGGCGCATCAACCAAGAACTACACCGGCGTGTGACCCCGAAGGGCCAGAGTATTGCG	723
OY	870	GCGCTCCGAGATCCGCCCCGAGGCCACCGGCTACCGGCGCTGTCTTTGTGGAGACGTG	929
Db	724	GCGCTCCGAGATCCGCCCCGAGGCCACCGGCTACCGGCGCTGTCTTTGTGGAGACGTG	783
OY	930	CTGAAGGACAAAGGCGGAGAGCTCAAGGGCAAGGCGCTGCGGTGTGCGCGCGGGCAAC	989
Db	784	CTGAAGGACAAAGGCGGAGAGCTCAAGGGCAAGGCGCTGCGGTGTGCGCGCGGGCAAC	843
OY	990	GTGGCCCAAGTACTCGCGGAGCTGCTCTGAGAGGGGCGCCATCGTGTGTGCTGTCC	1049

Db	844	GTGGGCCAGTACTGGCGGAGCTGCTGTGGAAAGGGCGGCATCTGTCTGTGGCTGTC	903
OY	1050	GACTTCCAGGGCTACTGTGTAGAGCCCAACGGCTTCACTCGCGAGACCTGACGGCGTG	11089
Db	904	GACTTCCAGGGCTACTGTGTAGAGCCCAACGGCTTCACTCGCGAGACCTGACGGCGTG	963
OY	1110	CAGGACATGAAGAAGAAACAACAGGGCCCGCATCTCCGAGTCAAGAGGGAACACGGCC	1165
Db	964	CAGGACATGAAGAAGAAACAACAGGGCCCGCATCTCCGAGTCAAGAGGGAACACGGCC	10223
OY	1170	GTGTATGTGGGCGACCGCGCGAAGCTTTGGGAGCTGAGCTGCAAGTGGACATCGCTTC	12259
Db	1024	GTGTATGTGGGCGACCGCGCGAAGCTTTGGGAGCTGAGCTGCAAGTGGACATCGCTTC	10833
OY	1230	CCCTGCGCCACCCAGAACGAGATCGATGAGACGACGCGCTGAGCTGTATCAAGCACGGC	12899
Db	1084	CCCTGCGCCACCCAGAACGAGATCGATGAGACGACGCGCTGAGCTGTATCAAGCACGGC	11434
OY	1290	TGCCAGTACGTGTGTGAGAGGGCGCCAACTGCCCTTCCACCAACGAGGCCATCAAAATAC	13459
Db	1144	TGCCAGTACGTGTGTGAGAGGGCGCCAACTGCCCTTCCACCAACGAGGCCATCAAAATAC	12033
OY	1350	AACAAGCGCGGCATCATCTACTGCCCGGCAAGGGCGGCAACGCGCGGCGGTGGCGGTC	14099
Db	1204	AACAAGCGCGGCATCATCTACTGCCCGGCAAGGGCGGCAACGCGCGGCGGTGGCGGTC	12653
OY	1410	AGCGGCTGTGAGATGACCCAGAACCCGATGAGCTTGAACTGTGACTGTGCGAGAGAGTTGCG	14659
Db	1264	AGCGGCTGTGAGATGACCCAGAACCCGATGAGCTTGAACTGTGACTGTGCGAGAGAGTTGCG	13233
OY	1470	GACAACTGTGAGAGCCGATCATGAAAGACATCTAACCATCTCCGCATGTGGGCGCTCCCGCAGA	15229
Db	1324	GACAACTGTGAGAGCCGATCATGAAAGACATCTAACCATCTCCGCATGTGGGCGCTCCCGCAGA	13833
OY	1530	TACAATGTGTAAGCTGTGCTGCGGGCGGCAACATCGCGGGCTTCAACCAAGTGGCTGATGCC	15899
Db	1384	TACAATGTGTAAGCTGTGCTGCGGGCGGCAACATCGCGGGCTTCAACCAAGTGGCTGATGCC	14433
OY	1590	GTCAAGGCCCAAGGGCGCTGTTTAAAGCTGCCAGAGCCCAAGCCACGCGCTCACCGGCAATCC	16499
Db	1444	GTCAAGGCCCAAGGGCGCTGTTTAAAGCTGCCAGAGCCCAAGCCACGCGCTCACCGGCAATCC	15099
OY	1650	AAC 1652	
Db	1504	AAC 1506	
RESULT 12			
US-10-627-886-23			
Sequence 23, Application US/10627886			
Publication No. US20040128710A1			
GENERAL INFORMATION:			
APPLICANT: Schmidt, Robert R.			
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES			
RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE			
DEHYDROGENASES AND METHODS OF USE			
NUMBER OF SEQUENCES: 26			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Saliwanchik & Saliwanchik			
STREET: 2421 N.W. 41st Street, Suite A-1			
CITY: Gainesville			
STATE: Florida			
COUNTRY: USA			
ZIP: 32606-6669			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/10/627,886			
FILING DATE: 24-Jul-2003			

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1      CLASSIFICATION: <Unknown>
2
3      PRIOR APPLICATION DATA:
4
5      APPLICATION NUMBER: 09/070,844
6
7      FILING DATE: 01-MAY-98
8
9      APPLICATION NUMBER: 08/725,596
10
11     FILING DATE: 03-OCT-96
12
13     APPLICATION NUMBER: 08/541,033
14
15     FILING DATE: 06-OCT-95
16
17     ATTORNEY/AGENT INFORMATION:
18
19     NAME: Lloyd, Jeff
20
21     REGISTRATION NUMBER: 35,589
22
23     REFERENCE/DOCKET NUMBER: UF-155CD3
24
25     TELECOMMUNICATION INFORMATION:
26
27     TELEPHONE: (352) 375-8100
28
29     TELEFAX: (352) 372-5600
30
31     INFORMATION FOR SEQ ID NO: 23:
32
33     SEQUENCE CHARACTERISTICS:
34
35     LENGTH: 1506 base pairs
36
37     TYPE: nucleic acid
38
39     STRANDEDNESS: double
40
41     TOPOLOGY: linear
42
43     MOLECULE TYPE: CDNA
44
45     FEATURE:
46
47     NAME/KEY: CDS
48
49     LOCATION: 4..1464
50
51     SEQUENCE DESCRIPTION: SEQ ID NO: 23:
52
53     GS-10-627-886-23

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Query Match	70.2%;	Score 1501.4;	DB 19;	Length 1506;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1502;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	150	AAGCGCGTCTTGCATGAGAGACAGATCTCCGCGATGAGCGCCACCGCGGACCTTCAAG	209	
Db	4	ATGCGCGCTCTCGCTGAGAGACAGATCTCCGCGATGAGCGCCACCGCGGACCTTCAAG	63	
QY	210	GCGCTGCAGAAAGGCGGTGTAACCAATGGCCCAAGGGGGGCACTGAAAGGCTGGTGCAC	269	
Db	64	GCGCTGCAGAAAGGCGGTGTAACCAATGGCCCAAGGGGGGCACTGAAAGGCTGGTGCAC	123	
QY	270	GGCATTAAGAAACCCCGGAGTGGCGGACGTGCTGACCGAGATCTTTCATGAAAGAACCCGGAG	329	
Db	124	GGCATTAAGAAACCCCGGAGTGGCGGACGTGCTGACCGAGATCTTTCATGAAAGAACCCGGAG	183	
QY	330	CAGCAGAGATTCAATGCAAGCGGTGGCGAGAGTGGCCGTCTCCCTGCGACCGCTGTTCCAG	389	
Db	184	CAGCAGAGATTCAATGCAAGCGGTGGCGAGAGTGGCCGTCTCCCTGCGACCGCTGTTCCAG	243	
QY	390	AAGGGCCCCGAGCGTGCATGCCCCATCTTCAAGCAGATCGTTGAGCCCTGAGCGGCTGATCAAC	449	
Db	244	AAGGGCCCCGAGCGTGCATGCCCCATCTTCAAGCAGATCGTTGAGCCCTGAGCGGCTGATCAAC	303	
QY	450	TTCCGCGGTCTCTGAGTGAAGCAGCGCGCGCAACTGCAGGTCAACCGGGGCTTCCGCGTG	509	
Db	304	TTCCGCGGTCTCTGAGTGAAGCAGCGCGCGCAACTGCAGGTCAACCGGGGCTTCCGCGTG	363	
QY	510	CAGTACTCTGTCGCGCATATGAGCCCTCAAGAGGCGGCTTGCAGCCCTTCCGTGAAC	569	
Db	364	CAGTACTCTGTCGCGCATATGAGCCCTCAAGAGGCGGCTTGCAGCCCTTCCGTGAAC	423	
QY	570	CTGTTCATCATGAGAGTCTCTTGCGCTTGGAGCAGATCTTCAAGAACAGCTTACCAACCTTG	629	
Db	424	CTGTTCATCATGAGAGTCTCTTGCGCTTGGAGCAGATCTTCAAGAACAGCTTACCAACCTTG	483	
QY	630	CCCATGAGGCGGCGCAAGAGGCGGCTTCCGACTTTCGACCCCAAGGGCAGAGCGCGGAG	689	
Db	484	CCCATGAGGCGGCGCAAGAGGCGGCTTCCGACTTTCGACCCCAAGGGCAGAGCGCGGAG	543	
QY	690	GTGATGAGCTTCTGCGACGTCTTTCATATACGAGGTGACGAGCGCCATCAGCTTACGTGAG	749	
Db	544	GTGATGAGCTTCTTCTGCGACGTCTTTCATATACGAGGTGACGAGCGCCATCAGCTTACGTGAG	603	
QY	750	GACGTGCGCGCGCGCAGCATTCGAGCGTGGGCGCGCGAGATTTGGCTACTTTTCGGCCAG	809	

Db 604 GACGTCGCGCGGCGATCGGCGTGGCGCGGCGAGATTGGTACTTTTGGCCAG 663  
Qy 810 TACAAAGCATCAACCAAGATCAACCGGCGTGTGACAGCCCGAAGGGCGAGATATGCG 869  
Db 664 TACAAAGCGCATCAACCAAGATCAACCGGCGTGTGACAGCCCGAAGGGCGAGATATGCG 723  
Qy 870 GAGTCGAGATCCGCGCGGAGCGCAACCGGCTACCGGCGCGTGTGTTGTGAGAACGTG 929  
Db 724 GAGTCGAGATCCGCGCGGAGCGCAACCGGCTACCGGCGCGTGTGTTGTGAGAACGTG 783  
Qy 930 CTGAAGGCAAGAGGCGAGCGCTCAAGGGCAAGCGCTGCTGTGTCTTGGCGCGGCAAC 989  
Db 784 CTGAAGGCAAGAGGCGAGCGCTCAAGGGCAAGCGCTGCTGTGTCTTGGCGCGGCAAC 843  
Qy 990 GTGGCCCACTACTGCGCGGAGCTGCTGTGAGAAAGGCGCGCATGCTGCTGCTGTC 1049  
Db 844 GTGGCCCACTACTGCGCGGAGCTGCTGTGAGAAAGGCGCGCATGCTGCTGCTGTC 903  
Qy 1050 GACTCCGAGGCTAGTGTAGAGCCCAACCGGCTTCAAGCGCGAGCGAGCTGCAAGCGGTC 1109  
Db 904 GACTCCGAGGCTAGTGTAGAGCCCAACCGGCTTCAAGCGCGAGCGAGCTGCAAGCGGTC 963  
Qy 1110 CAGGACATGAAGAAAGAAACAAACAGCGCGCGCATCTCGAGTACAAAGAGCAACCGCC 1169  
Db 964 CAGGACATGAAGAAAGAAACAAACAGCGCGCGCATCTCGAGTACAAAGAGCAACCGCC 1023  
Qy 1170 GTGTATGTGGCGGACCGCGGCAAGCTTGGAGAGCTGAGCTGCGAGTGAACATGCGCTTC 1229  
Db 1024 GTGTATGTGGCGGACCGCGGCAAGCTTGGAGAGCTGAGCTGCGAGTGAACATGCGCTTC 1083  
Qy 1230 CCCTGCGCGCACCGAAAGAGATGATGAGCAACCGCGCGAGCTGTATGAAGAGCGG 1289  
Db 1084 CCCTGCGCGCACCGAAAGAGATGATGAGCAACCGCGCGAGCTGTATGAAGAGCGG 1143  
Qy 1290 TGCCAGTACTGTGTGAGAGGCGGCAACATGCGCTTCAACCAAGAGCGCATCAAGATAC 1349  
Db 1144 TGCCAGTACTGTGTGAGAGGCGGCAACATGCGCTTCAACCAAGAGCGCATCAAGATAC 1203  
Qy 1350 AACCAAGCGCGCATCTACTTGTGCGCGGCAAGGCGGCAACCGCGCGGCGTGGCGGTC 1409  
Db 1204 AACCAAGCGCGCATCTACTTGTGCGCGGCAAGGCGGCAACCGCGCGGCGTGGCGGTC 1263  
Qy 1410 AGCGGCGTGTGAGATGAGCAACCGCATGTAGCGCTGAACTGTGAGAGAGGTTGCG 1469  
Db 1264 AGCGGCGTGTGAGATGAGCAACCGCATGTAGCGCTGAACTGTGAGAGAGGTTGCG 1323  
Qy 1470 GACAAGCTGAGCGCATCATGAAGACATCTACGACTCGGCATAGGGCGCTCCGCGAGA 1529  
Db 1324 GACAAGCTGAGCGCATCATGAAGACATCTACGACTCGGCATAGGGCGCTCCGCGAGA 1383  
Qy 1530 TACAATGTGACTGTGCTGCGGCGCGCAACATCGCGGCGCTTCAACCAAGTGGCTGATGCC 1589  
Db 1384 TACAATGTGACTGTGCTGCGGCGCGCAACATCGCGGCGCTTCAACCAAGTGGCTGATGCC 1443  
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Db 1444 GTCAAGGCGCGAGCGCTGTGTTAAGCTGCCAAGGCGCAAGCGAGCTCACCGGCAATCC 1503  
Qy 1650 AAC 1652  
Db 1504 AAC 1506

## RESULT 13

US-09-070-844-25  
: Sequence 25, Application US/09070844  
: Patent No. US20020062495A1  
: GENERAL INFORMATION:  
: APPLICANT: Schmidt, Robert R.  
: APPLICANT: Miller, Philip  
: TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
: TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE

; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,844  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UP155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1473 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 4..1431  
; US-09-070-844-25  
Query Match 68.7%; Score 1470; DB 9; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 483 CTGAGGTCAACCGCGGCTTCCGCGTCACTGCTCCGCAATCGGCGCTTCAAGAGGC 542  
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Db 1444 GCCCAAGCGAGCTCAACCGGCAATCCAA 1473  
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RESULT 14

US-10-627-886-25  
; Sequence 25, Application US/10627886  
; Publication No. US20040128710A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Robert R.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
; RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE  
; DEHYDROGENASES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/627,886  
; FILING DATE: 24-Jul-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/070,844  
; FILING DATE: 01-MAY-98  
; APPLICATION NUMBER: 08/725,596  
; FILING DATE: 03-OCT-96  
; APPLICATION NUMBER: 08/541,033  
; FILING DATE: 06-OCT-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lloyd, Jeff  
; REGISTRATION NUMBER: 35,589  
; REFERENCE/DOCKET NUMBER: UF-155CD3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1473 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 4..1431  
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-10-627-886-25  
  
Query Match 68.7%; Score 1470; DB 19; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 183 ATGAGCGCCACACCGCGGCACTTCAAGGCGCTCAGAGGCGGTGAAGAGAGTGGCCACC 242  
|||  
Db 4 ATGAGCGCCACACCGCGGCACTTCAAGGCGCTCAGAGGCGGTGAAGAGAGTGGCCACC 63  
|||  
QY 243 AAGCGGCGCACTAGAGGCGTGTGCAAGGCGATCAAGAACCCGAGCTGCCAGCTGCTG 302  
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Db 64 AAGCGGCGCACTAGAGGCGTGTGCAAGGCGATCAAGAACCCGAGCTGCCAGCTGCTG 123  
|||  
QY 303 ACCGAGATCTTCAAGAGAACCCGAGAGCAGAGAGTTCATGCAAGCGGTGCCAGAGTG 362  
|||  
Db 124 ACCGAGATCTTCAAGAGAACCCGAGAGCAGAGAGTTCATGCAAGCGGTGCCAGAGTG 183  
|||  
QY 363 GCGGTCTCTGAGAGCGCGGTTCGAGAGAGCGCGGAGAGTGTGCGCCATCTTCAAGCAG 422  
|||  
Db 184 GCGGTCTCTGAGAGCGCGGTTCGAGAGAGCGCGGAGAGTGTGCGCCATCTTCAAGCAG 243  
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QY	423	ATCGTTGAGCCGTGAAGGGGTATCATCACTTCGCGGTGCTCTGGCTGTGAAGAGCGCCGGCAAC	482
Db	244	ATCGTTGAGCCGTGAAGGGGTATCATCTTCGCGGTGCTCTGGCTGTGAAGAGCGCCGGCAAC	303
QY	483	CTGCAGGTCAACCGCGGCTTCGCGGTGAAGTACTGTCCGCGCATGTGGCCCTTACAAGGGG	542
Db	304	CTGCAGGTCAACCGCGGCTTCGCGGTGAAGTACTGTCCGCGCATGTGGCCCTTACAAGGGG	363
QY	543	GCGCTGCGCTTCACCCCTCCGTGAACCTGTCCATCATGAAGTTCTTTGCCCTTTGAGCAG	602
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QY	603	ATCTTCAAGAAACAGCTGAACCACTTCGCCCATMGGGGCGCGCAAGAGGGGGCTCCGCACTTC	662
Db	424	ATCTTCAAGAAACAGCTGAACCACTTCGCCCATMGGGGCGCGCAAGAGGGGGCTCCGCACTTC	483
QY	663	GACCCCAAGGGCAAGAGGAGCGCGGAGGTGATGCCTTCTGCGACTCTCTTCAATGAACCGAG	722
Db	484	GACCCCAAGGGCAAGAGGAGCGCGGAGGTGATGCCTTCTGCGACTCTCTTCAATGAACCGAG	543
QY	723	CTGCACGCGCCACATCAGCTACGTGCGAGGACGTGCCCGCGCGGACATCGCGGTGGGCGCG	782
Db	544	CTGCACGCGCCACATCAGCTACGTGCGAGGACGTGCCCGCGCGGACATCGCGGTGGGCGCG	603
QY	783	CGCGAGATTGGGCTACCTTTTGGCCAGTACAAAGCGCATCACCAGAACTAACCCGGCTG	842
Db	604	CGCGAGATTGGGCTACCTTTTGGCCAGTACAAAGCGCATCACCAGAACTAACCCGGCTG	663
QY	843	CTGAACCCCGAAGGGGCGAGAGTATGGCGGCTCCGAGATCCGCGCCGAGGGCCACCGGGCTAC	902
Db	664	CTGAACCCCGAAGGGGCGAGAGTATGGCGGCTCCGAGATCCGCGCCGAGGGCCACCGGGCTAC	723
QY	903	GCGCGCGGTCTGTTTGTGGAAGAACGTGCTGAAGGACAAAGGGCGAGAGCCTCAAGGGCAAG	962
Db	724	GCGCGCGGTCTGTTTGTGGAAGAACGTGCTGAAGGACAAAGGGCGAGAGCCTCAAGGGCAAG	783
QY	963	CGCTGCTCTGTGTCTGCGCGCGGGCAAGCTGGGCCCACTACTGCGCGGAGCTGTCTGGAG	1022
Db	784	CGCTGCTCTGTGTCTGCGCGCGGGCAAGCTGGGCCCACTACTGCGCGGAGCTGTCTGGAG	843
QY	1023	AAGGGCGGCATCGTGCCTGCTGCCGACTCCGAGGGCTAGGTGTAAGAGCCCAAGGGG	1082
Db	844	AAGGGCGGCATCGTGCCTGCTGCCGACTCCGAGGGCTAGGTGTAAGAGCCCAAGGGG	903
QY	1083	TTCAACGCGCGAGCAGCTGCGCGGTGCGAGCATGAAGAAAGAAAGAACAAAGCGGCCCGC	1142
Db	904	TTCAACGCGCGAGCAGCTGCGCGGTGCGAGCATGAAGAAAGAAAGAACAAAGCGGCCCGC	963
QY	1143	ATCTTCGAGTACAAAGGCGACACGCGCGTGTATGTGGCGAACCAGCGCAAGCCTTTGGAG	1202
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QY	1203	CTGGAACGGCCAGGTGAGATAGCCCTTCCCTTCGCGCACCCCAAGAACGAAATGATGATGAC	1262
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Db	1084	GACGCCGAGCTGTGATCAAGCAAGCTGCGCAGTACTGTGTGAGAGGGGCGCAACTGCGCC	1143
QY	1323	TCACACCAAGAGGCCATTCACAAAGTACAAAGAGCGGCAATCATCTAGCCCGGCAAG	1382
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QY	1383	GCGGCGCAACGCGCGGCGGTGGCGGTCAAGCGGCTGTGAGATGATCCCAAGATCCGATGAGC	1442
Db	1204	GCGGCGCAACGCGCGGCGGTGGCGGTCAAGCGGCTGTGAGATGATCCCAAGATCCGATGAGC	1263
QY	1443	CTGAACCTGGAATCTGCGAGAGAGTTTCGCAACAAGCTGAGCGCATCATGAAGACATCTAC	1502
Db	1264	CTGAACCTGGAATCTGCGAGAGAGTTTCGCAACAAGCTGAGCGCATCATGAAGACATCTAC	1323
QY	1503	GACTTCGCGCATATGGGGCGTCCCGCAGATTAACATGTTGACTGTGGCTGGGGCGCAACATC	1562

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Db      1324 GACTTCGGCATGGGCGCTCCCGAGATACATATTGACTCTGGCTGGCGGCGCAATC 1383
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RESULT 15
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; Sequence 30503, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zvekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H
; TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: Eultra.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30503
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-30503

Query Match      27.6%; Score 590.8; DB 17; Length 1338;
Best Local Similarity 68.1%; Pred. No. 1.5e-132; Indels 18; Gaps 4;
Matches 887; Conservative 0; Mismatches 397;

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Db      46 GATCCCGATCAGCCCGCAATTCCACAGCGGTGGAAGAGGTGCTGCGTTCCTTGCGCG 105
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy      381 GTGTTGAGAGAGCGCCCGGACGCTGTG-----CCATCTTCAAGAGATGCTTGAAGCTT 434
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 435 GAGCGCTGATCACTTCCGCGTGTCTGCGTGCAGCAGCCGCGCAACTGCAAGTCAAC 494  
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QY 495 GCGGCTTCCGCGTGCAGTACTCGTCCGCATTCGGCCCTTACAGAGCGCGCTGCGCTTC 554  
DB 226 CTGTGGCTACCGGGTGCAGATGAGCAGCGCCATCCGCCCTTACAGAGCGCGCTGCGCTTC 285  
QY 555 CACCCCTCCGTGAACCTGTCCATCATGAGTCTCTGCGCTTGGGAGATCTTCAAGAAC 614  
DB 286 CATCTCTGGTCAACTCGGGGTGTCTGAGTCTCTGCGCTTCAAGAGTCTTCAAGAAC 345  
QY 615 AGCTTGACCAACCTGCCCCATGAGCGCGCGCAAGGCGCGCTCCGACTTCAACCCCAAGGCG 674  
DB 346 TCCCTGACCACTCTGCCCATGAGCGCGCGCAAGGCGCGCTCCGACTTCAAGAGGCG 405  
QY 675 AAGAGCGAGCGGAGTGTGCGCTTCTGCGGATCTTCAATGACCGAGCTGCAGCGCCAC 734  
DB 406 AAGAGCGAGCGCGGAGTGTGCGCTTCTGCGGATCTTCAATGAGCGAGCTGTACCGCCAC 465  
QY 735 ATGAGCTACGTCGAGGAGCGTGCAGCGCGCGCGGACATCGCGCGGCGCGCGGAGATTGGC 794  
DB 466 GTCCGCGCGCGAGCTGACGTCGCGCGCGCGCGGACATCGCGCGGCGCGGAGATTGGC 525  
QY 795 TACCTTTCCGCGCAGTACCAAGCGCATCACAGAACTACAACCGCGGTGTGACCCCGAAG 854  
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QY 855 GCGCGAGAGTATGGCGGCTCCGAGATCCGCCCGAGGCGACCGGCTACCGCGCGCTGCTG 914  
DB 586 GCGCTGAGCTATGGCGGCGAGCTGATCCGCCGAGGCGACCGGCTTCCGCTGCGTCTAC 645  
QY 915 TTTGTGAGAACGTCGTGAAGGAGCAAGGGGAGAGCCCTCAAGGGGCAAGCGCTGCTG 974  
DB 646 TTCCGCCAGGAATGCTCAAGAGATCTGAGCCGCGCTTCAAGGCGAGCGGCGGAGTGC 705  
QY 975 TCTGCGCGCGGCAAGTGCAGTACGCGGAGGCTGCTGAGAAAGGCGCCATC 1034  
DB 706 TCCGCGCTCGGCGCAAGTGCAGTACGCGCGCGCGCAAGGTCATGAAATGGCGCGCAAG 765  
QY 1035 GTGCTGTGCTGTCCGACTCCAGGCGTACGTTACAGAGCCCAAGCGCTTCAAGCGCGAG 1094  
DB 766 GTGATCTGCTGTCCGATTCGAAAGGCACTGTATGCCGAGCGGCGCTTCCGAGAG 825  
QY 1095 CAGCTGAGGCGGTGAGGAGCATGAGAAAGAAACAAGCGCGCCGATCTCCGAGTAC 1154  
DB 826 CAGTGGGAATACGTGATGAGCTGAAAGACGTG--CGCGCGGCGGATCTCCGAGATG 882  
QY 1155 AAGAGCGACACCGCGGTATGTGGGAGACCGCGCAAGCTTGGAGCTGAGTGCAG 1214  
DB 883 GCGGAGCAGTTTCTCGGAGTTTCTGAAAGGCGCGCGCTTGGGCTTGGCTGC--- 939  
QY 1215 GTGAGCATCGCTTTCCTGCGCGCAACCCAGAAAGAGATCGATGAGCAGCGCGAGCTG 1274  
DB 940 ---GATATCGGCTGCGCTTGGCGCAACCCAGAAAGAGATGCGAGGATGCGCGCGC 996  
QY 1275 CTGATCAAGCAAGCGCTGCGAGTACGTGTGAGAGGCGCGCAAGCGCTTCAACCAAGAG 1334  
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QY 1395 GCGGCGGTGGGCTCAGCGGCGCTTGAAGATGACCAAGAACCGCATGAGCTGAACTGACT 1454  
DB 1117 GCGGCGGTGGGCTGAGCGGCGCTTGAAGATGTCGAGAACCGCATGCGCTGCTTGAAGC 1176  
QY 1455 CGGAGAGAGTTTCCGCAAGAGCTGAGCGATCATGAAAGCAATCTAGACTCCGCGATG 1514  
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QY 1515 GAGCGCTCCGAGATA---CAATGTTGACTGCGCGCGCGCGCAACATCGCGGCTTC 1571  
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QY 1572 ACCAAGTGTGATGCTGCAAGGCGCGCAAGGCGCTGTTAA 1613  
DB 1297 GTCAAGTGTGCGATGCGATGCGCGCGCGCGGCTGTA 1338

Search completed: July 10, 2005, 00:07:50  
Job time : 1216 secs



GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: July 9, 2005, 18:15:07 ; Search time 6261 Seconds

(without alignments)  
13010.308 Million cell updates/sec

Title: US-10-627-886-1

Perfect score: 2140

Sequence: 1 CTCCTTCTGCTGCCCTCT.....AAAAAAAAAAAAAAAAAAAA 2140

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_est4:\*

5: gb\_est5:\*

6: gb\_est6:\*

7: gb\_est7:\*

8: gb\_est8:\*

9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	395.6	18.5	1245	8	BZ569675 pac82-164
2	385	18.0	1123	8	BZ569676 pac82-164
3	358.2	16.7	922	8	BZ578032 m812_5687
4	350.2	16.4	898	7	CV219575 EST879285
5	323.6	15.1	778	7	CV211069 EST870779
6	305.6	14.3	1114	9	CNS060DN
7	292.4	13.7	854	5	BM480553
8	288.6	13.5	943	7	CV211068
9	282.8	13.2	540	1	AU186881
10	281	13.1	820	9	CL693787 PRI0162C
11	274.6	12.8	638	7	CF839891
12	271.6	12.7	727	5	BM436105
13	270	12.6	694	5	BM438709
14	269	12.6	730	5	BM475527
15	266	12.4	527	1	AU196696
16	264.4	12.4	790	7	CF693234
17	264.4	12.3	835	7	CF709188
18	263.4	12.3	836	7	CF717421
19	262.8	12.3	811	7	CF704125
20	262.8	12.3	815	7	CF678148
21	262.8	12.3	817	7	CF715582
22	262.8	12.3	820	7	CF676255
23	262.8	12.3	826	7	CF687048
24	262.8	12.3	826	7	CF711744

25	262.8	12.3	833	7	CF695795
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31	262.8	12.3	845	7	CF699111
32	262.8	12.3	845	7	CF706882
33	262.8	12.3	847	7	CF690384
34	262.8	12.3	848	7	CF707240
35	262.8	12.3	853	7	CF718447
36	262.8	12.3	859	7	CF708923
37	262.8	12.3	860	7	CF687244
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42	262.8	12.3	870	7	CF694123
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## ALIGNMENTS

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DEFINITION	pac82-164_965, genomic survey sequence.				
ACCESSION	BZ569675				
VERSION	BZ569675.1	GI:27204622			
KEYWORDS	GSS.				
SOURCE	Pseudomonas aeruginosa				
ORGANISM	Pseudomonas aeruginosa				
REFERENCE	1 (bases 1 to 1245)				
AUTHORS	Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.				
TITLE	Whole-Genome-Sequence Variation among multiple isolates of Pseudomonas aeruginosa library				
JOURNAL	J. Bacteriol. (2002) In press				
COMMENT	Contact: Chris K. Raymond Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, USA Tel: 2062216954 Fax: 2066857244 Email: craymond@u.washington.edu Class: Shotgun.				
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Best Local Similarity	74.2%; Pred. No. 1,4e-68;				
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Db	29 TTCGCGTGTCTGCTGACGACGCCGCGGTACGCGTCAACCTGCTACCGCGGAT 88				
Oy	510 CAGTACTGTCTGCGCATCGGCCCTTACAGAGGCGGCGCTTCCACCCCTCCGTGAC 569				

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Db      89  CAGATGAGCAGCGCCATCGGCCCTACAAAGGCGGCTCGGCTTCATCCCTCGGTCAAC 148
Qy      570 CTGTCCATCATGAAGTCTCTGCTTTGAGAGATCTTTCAGAGACAGCTGACCACTCG 623
Db      149 CTCGGGGGTGGAAGTCTCTGCTTCGAGAGAGGTCTTCAAGAACTCCCTGACCACTCG 208
Qy      630 CCATGAGGCGGCGGCAAGGCGGCTCGCATTCGACCCCAAGGCGCAAGAGCGCGAG 689
Db      209 CCATGAGGCGGCGGCAAGGCGGCTCGCATTCGACCCCAAGGCGCAAGAGCGCGAG 268
Qy      690 GTGATGCGCTTCTGCGAGTCTTTCATGACCGAGCTGACGCGCACTACAGTACGTGAG 749
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Qy      750 GACGTCGCGGCGGCGGCAATGCGGCTGAGCGCGCGGCGGCAATGCGGCTGAGCGGCGAG 809
Db      329 GACGTCGCGGCGGCGGCAATGCGGCTGAGCGCGCGGCGGCAATGCGGCTGAGCGGCGAG 388
Qy      810 TACAAGCGCATCACCAAGAACTACACCGGCGGTGCTGACCCCGAAGGCGCAAGATATGCG 869
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Qy      870 GGTCTCCGAGATCCGCGCGGCGGCAAGCGGCTGACCGGCGGCTGCTGTTTGAGAGACGTG 929
Db      449 GCGAGCATGATCCGCGCGGCGGCAAGCGGCTGACCGGCGGCTGCTGTTTGAGAGACGTG 508
Qy      930 CTGAAGAGCAAGGCGGCGGCGGCAAGGCGGCTGAGCGGCGGCTGAGCGGCGGCGGCAAC 989
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Qy      990 GTGCGCCAGTACTGCGCGGCGGCGGCTGAGCGGCGGCGGCAAGCGGCGGCGGCGGCGGCGG 1049
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Qy      1050 GACTCCGAGGCTGACTGTAAGAGCCCAAGCGGCTTCAAGCGGCGGCGGCAAGCGGCGGCGG 1109
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Qy      1110 CAGGACATGAAGAA 1123
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RESULT 2
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ACCESSION      B2569676
VERSION      B2569676.1 GI:27204626
KEYWORDS      GSS.
SOURCE      Pseudomonas aeruginosa
ORGANISM      Pseudomonas aeruginosa
REFERENCE      Pseudomonas aeruginosa
AUTHORS      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
TITLE      Pseudomonadaceae; Pseudomonas.
JOURNAL      1 (bases 1 to 1123)
COMMENT      Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
            Burns,J.L., Kaul,R. and Olsen,M.V.
            Whole-Genome-Sequence Variation among multiple isolates of
            Pseudomonas aeruginosa library
            J. Bacteriol. (2002) In press
            Contact: Chris K. Raymond
            Genome Center
            University of Washington
            Box 352145, Seattle, WA 98105-2145, USA
            Tel: 2062216954
            Fax: 2066857244
            Email: craymond@u.washington.edu
            Class: shotgun.
FEATURES
            1..1123
            Location/Qualifiers
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/strain="2-164"
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Query Match      18.0%; Score 385; DB 8; Length 1123;
Best Local Similarity 72.8%; Pred. No. 1.8e-66;
Matches 496; Conservative 0; Mismatches 185; Indels 0;

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Qy      510 CAGTACTGTCCGCGCATCGGCGGCTTCAAGAGGCGGCGGCTTCCGCGTGAAC 569
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Qy      570 CTGTCCATCATGAAGTCTCTGCTTTGAGAGATCTTCAAGAACTCCCTGACCACTCG 629
Db      158 CTGCGGCTGTGAAGTCTCTGCTTTGAGAGATCTTCAAGAACTCCCTGACCACTCG 217
Qy      630 CCATGAGGCGGCGGCAAGGCGGCTGCGACTTCAAGCGGCGGCGGCAAGAGCGAGCGGAG 689
Db      218 CCATGAGGCGGCGGCAAGGCGGCTGCGACTTCAAGCGGCGGCGGCAAGAGCGAGCGGAG 277
Qy      690 GTGATGCGCTTCTGCGAGTCTTTCATGACCGAGCTGACGCGCACTACGTAAGTACGTGAG 749
Db      278 GTGATGCGCTTCTGCGAGTCTTTCATGACCGAGCTGACCGCGCACTACGTAAGTACGTGAG 337
Qy      750 GAGTGTCCGCGGCGGCAAGTGTGCGGCGGCGGCGGAGTTGAGTAACTTTCCGCGAG 809
Db      338 GAGTGTCCGCGGCGGCAAGTGTGCGGCGGCGGCGGAGTTGAGTAACTTTCCGCGAG 397
Qy      810 TACAAGCGCATCAACCAAGAACTACACCGGCGGCTGACCCCGAAGGCGGCAAGTATGCG 869
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Db      458 GGTCTCCGAGATCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 517
Qy      930 CTGAAGAGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 989
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Qy      1050 GACTCCGAGGCTGACTGTAAGAGCCCAAGCGGCTTCAAGCGGCGGCGGCGGCGGCGG 1109
Db      638 GATTCGGAAGTCACTGCTATGCGAGGCGGCGGCGGCTTCCGAGGAGTGAATATCTG 697
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Db      698 ACTGAATGAGCTGAAGAAC 718

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RESULT 3
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LOCUS      B2578032
DEFINITION      msh2_5687.y2 msh Pseudomonas aeruginosa genomic clone msh2_5687,
ACCESSION      B2578032
VERSION      B2578032.1 GI:27213093
KEYWORDS      GSS.
SOURCE      Pseudomonas aeruginosa
ORGANISM      Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Pseudomonadaceae; Pseudomonas.  
1 (bases 1 to 922)  
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,  
Burns,J.B., Kaul,R. and Olsen,M.V.  
Whole-Genome-Sequence variation among multiple isolates of  
Pseudomonas aeruginosa library  
J. Bacteriol. (2002) In press  
Contact: Chris K. Raymond  
Genome Center  
University of Washington  
Box 352145, Seattle, WA 98105-2145, USA  
Tel: 2062216954  
Fax: 2066857244  
Email: craymond@u.washington.edu  
Class: shotgun

FEATURES  
source  
Location/Qualifiers  
1..922  
/organism="Pseudomonas aeruginosa"  
/mol\_type="genomic DNA"  
/strain="MSH"  
/db\_xref="taxon:287"  
/clone="msb2\_3687"  
/clone\_1id="msb"  
/note="Environmental isolate. Whole genomic shotgun  
library."

ORIGIN

Query Match 16.7%; Score 358.2; DB 8; Length 922;  
Best Local Similarity 72.2%; Pred. No. 4,1e-61;  
Matches 480; Conservative 0; Mismatches 180; Indels 5; Gaps 1;

410 CATTTCAAGAGATCTGTGAGCTTGAGCGGTGATCACTTCCGCGTCTGGCTGA 469  
101 CATCATTTAAGCATCGTCGAAACCGAGCGGCGCATCTGTCCGCGTACCTGAGT 160  
470 CGAGCGCGGCAACTGCAAGTCAACCGCGCTTCGCGTCACTGCTCCGCGCATCG 529  
161 CGACGAGGCGCGGTGACGCGTCAACCGTGTACCGGTGATGAGCAGCGCATCG 220  
530 CCGCTCAAGGCGCGCTGCGCTTCAACCGCTCGTGAACCTGTTCATGAAATCT 589  
221 CCGCTCAAGGCGCGCTGCGCTTCAACCGCTCGTGAACCTGTTCATGAAATCT 280  
590 TCGCTTGAAGATCTTCAAGAACGCTTCAACCGTTCGCGTGGCGCGCGCAAGG 649  
281 CGCTTGAAGATCTTCAAGAACGCTTCAACCGTTCGCGTGGCGCGCGCAAGG 340  
650 CGGCTCGCATTCGACCCCAAGGCGAGGCGAGCGGAGGTGATGCGCTTCTGCGATC 709  
341 CGGCTCGCATTCGACCCCAAGGCGAGGCGAGGCGAGGTGATGCGCTTCTGCGATC 400  
710 CTTGATGACCGAGCTGACGCGCATCATGCTAGTGAAGACGTCGCCGCGCGCAT 769  
401 GTTCATGAGGAGTGTGACGCGCATCATGCTAGTGAAGACGTCGCCGCGCGCAT 460  
770 CGGCTGAGGCGCGCGCGAGTGGCTTTCGCGCGAGTGAAGGCGCATCAAGAA 829  
461 CGGCTGAGGCGCGCGCGAGTGGCTTTCGCGCGAGTGAAGGCGCGCATCAAG 520  
830 CTTACGCGGCTGCTGACCCCGAAGGCGAGGATGATGCGCGCTCCGAGATCGCGCG 889  
521 GTTCATCTCGGTGCTGACCGCGAGGCGCTGAGCTATGAGCGCGCGCATCAAG 580  
890 GCGCAGCGGCTGACGCGCGCGTGTGTTGAGAGACGTGCTGAAGACAAAGGCGAG 949  
581 GCGCAGCGGCTTGTGCTGCGCTGCTGCGCGCGAGAAATGCTTGAAGATGCTGCG 640  
950 CTTCAAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1009  
641 CTTTACGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 695  
1010 GCTGCTGAGAGAGGCGCGCATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069

Db 696 GCGCAAGTATGAGAAATGCGCGAGTATCGCTGCTCCGATTTGAGACGCTGATG 755

Qy 1070 CGAGC 1074

Db 756 CGAGC 760

RESULT 4  
CV219575  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CV219575 898 bp mRNA linear EST 16-SEP-2004  
EST879285 non-normalized T1 cDNA library Trichomonas vaginalis cDNA  
clone T1VCY21 5' end, mRNA sequence.  
CV219575  
CV219575.1 GI:5216555  
EST.  
Trichomonas vaginalis  
Trichomonas vaginalis  
Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;  
Trichomonadidae; Trichomonadinae; Trichomonas.  
1 (bases 1 to 898)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Carlton,J.M., Dyall,S., Johnson,P.J. and Frazer,C.M.  
The complete genome sequence of the sexually transmitted parasite  
Trichomonas vaginalis  
Unpublished (2004)  
Other ESTs: EST879284  
Contact: Jane Carlton  
Parasite Genomics Group  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-530-9319  
Fax: 301-838-0208  
Email: carlton@igr.org  
Seq primer: lambda Triplex2.  
Location/Qualifiers  
1..898  
/organism="Trichomonas vaginalis"  
/mol\_type="mRNA"  
/strain="T1"  
/db\_xref="taxon:5722"  
/clone="T1VCY21"  
/clone\_1id="non-normalized T1 cDNA library"  
/note="Vector: Lambda Triplex2; Site 1: SfiA; Site 2:  
SfiB; T. vaginalis strain T1 library constructed from  
cDNA, made in lambda Triplex2. Inserts cloned  
unidirectionally in the SfiA and SfiB sites. Mass excision  
of library produced inserts in pTriplex2 plasmid. Inserts  
sequenced from both 5' and 3' ends using Triplex2  
sequencing primer and polydT 24 bp primer respectively."

ORIGIN

Query Match 16.4%; Score 350.2; DB 7; Length 898;  
Best Local Similarity 64.8%; Pred. No. 1,1e-59;  
Matches 520; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

Qy 321 GACCGGAGAGAGAGATTCAGGCGCGGTGCGAGGTCGCGCTCCGACACCC 380  
Db 58 GATTCAGATGAGAGATTCAGGCGCGGTGCGAGGTCGCGCTCCGACACCC 117  
381 GTGTTGAGAGAGCGCGCGAGTGTGCGCATCTTCAAGAGATCGTTGAGCGCGC 440  
Db 118 ATCTTGAGAGAGAGCGCGAGTGTGCGCATCTTCAAGAGATCGTTGAGCGCG 177  
441 GTATGACCTTCCGCGTGTGCGCGTGTGCGCGAGCGCGCGCACTGCGATCAACGCG 500  
178 GTATGACCTTCCGCGTGTGCGCGTGTGCGCGAGCGCGCGCACTGCGATCAACG 237  
Qy 501 TTCCGCGTGAAGTCTGCGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 560  
Db 238 TTCCGCGTGAAGTCTGCGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 297  
561 TCCGTAACCTGTCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 620  
Db 298 AACGTTAACCCTTTCATCCTCAGGTTCTGCTTGGAGAGAGTTTCAAGAACTCAT 357

QY 621 ACCACCTGCCCATTGGGCGGCGGCAAGGCGGCTCCGACTTCGACCCCAAGGCGAAGGC 680  
Db 358 ACAACACTCCCAATGGGATGGGCAAGGGATGGTTCCGATTTTCGACCCAGCGGCAATCT 417  
QY 681 GACCGGAGGATGATCGCTTTCGCACTCTTATGACCGAGCTGCAGCGCCACATCAAC 740  
Db 418 GATGGCCAAAGTCAAGAAATTCCTGCGAGTCTTCATGCTCGAACTCCAGCGCCACATCGGC 477  
QY 741 TAGTGGAGGACGCGCCGCGGAGACATGGCGGTGGGCGGCGGAGATTGGCTACTCT 800  
Db 478 GCGAACACAGATGTCCTCAAGCTGTGATATCGGTCTCGTGAATCGGCTACATG 537  
QY 801 TTCGGCCAGTACCAAGCCCATCACAAGAACTACACCGCGCTGTGACCCCGAAGGCGCAG 860  
Db 538 TTCGGCCAGTACCAAGCCCATCACAAGAACTACACCGCGCTGTGACCGGCAAGGGATC 597  
QY 861 GAGTATGCGCGCTCCGAGATCGCCCGAGGCAACCGGCTACGCGCGCTGCTGTTTGTG 920  
Db 598 CCATACCGTGGCTCACTGATCCGTCCAGAAAGCTACAGGCTACGGTCTTGTCTACTGTC 657  
QY 921 GAGAACGCTGAGAGCAAGAGGCGAGAGACCTCAAGGCGCAAGCGCTGCTGTGCTGTC 980  
Db 658 ACAGAAATGCTCCGTGCTAAGGCGCAAGAGATCAAGGCGCAAGCGCTGCTGTGCTGTC 717  
QY 981 GCGGCGCAAGTGGCCCACTACTGCGCGAGCTGCTGTGAGAAAGGCGCGCATGCTG 1040  
Db 718 TCCGCGCAAGTGGCGCAAGTACTGCTGCGCAAGAGCTCAAGCGCTGCGGCGCAATCCGATC 777  
QY 1041 TCGCTGTCCAGCTCCCAAGGCTACGTGATGAGCGCCAAAGCGCTTACGCGGAGCAGCTG 1100  
Db 778 TCATGCTCAGACTCACAAGCGCTCTCATCTTCAGGATGATGACAAAGSACATCTT 837  
QY 1101 CAGGCGGTGAGAGCATGAAGA 1123  
Db 838 GATGCTGTCACTGACATCAAGA 860

RESULT 5 778 bp mRNA linear EST 16-SEP-2004  
CV211069  
LOCUS EST870779 non-normalized T1 cDNA library Trichomonas vaginalis cDNA  
DEFINITION  
CV211069  
VERSION CV211069.1 GI:52158049  
KEYWORDS EST.  
SOURCE Trichomonas vaginalis  
ORGANISM Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;  
Trichomonadidae; Trichomonadinae; Trichomonas.  
REFERENCE 1 (bases 1 to 778)  
AUTHORS Carlton, J.M., Pyall, S., Johnson, P.J. and Fraser, C.M.  
TITLE The complete genome sequence of the sexually transmitted parasite Trichomonas vaginalis  
JOURNAL Unpublished (2004)  
COMMENT Other ESTs: EST870778  
Contact: Jane Carlton  
Parasite Genomics Group  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-9319  
Fax: 301-838-0208  
Email: carlone@igr.org  
Seq primer: lambda Triplex2.  
FEATURES  
SOURCE Location/Qualifiers  
1..778  
/organism="Trichomonas vaginalis"  
/mol\_type="mRNA"  
/strain="T1"  
/db\_xref="taxon:5722"  
/clone="T1VBE13"  
/clone\_id="non-normalized T1 cDNA library"  
/note="Vector: Lambda Triplex2; Site\_1: SfiA; Site\_2:

SfiB, T. vaginalis strain T1 library constructed from cDNA, made in lambda Triplex2. Inserts cloned unidirectionally in the SfiA and SfiB sites. Mass excision of library produced inserts in pTriplex2 plasmid. Inserts sequenced from both 5' and 3' ends using Triplex2 sequencing primer and polydT 24 bp primer respectively."

ORIGIN  
Query Match 15.1%; Score 323.6; DB 7; Length 778;  
Best Local Similarity 65.8%; Pred. No. 3,3e-54;  
Matches 470; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

QY 321 GACCGGAGCAGAGAGTTCATGACGCGCGCGGAGGTGCGCTTCCTGACGCC 380  
Db 58 GATCCAGATCAGAGGAATTCATCCAGAGCTCAGAGAAATTCATCTCGTCCCA 117  
QY 381 GTGTTGAGAGAGCGCCCGAGCTGCTGCCATCTTCAAGCATGCTTGAGCTGAGCC 440  
Db 118 ATCTCGAGAGAGAACCAAGTACAGAAAGCTCTCCAGCTCTTGTGAGCAGAGCT 177  
QY 441 GTGATCACTTCGCGGTCTGCTGAGACGCGCGCAACCTGACAGTCAACGCGG 500  
Db 178 GTTATCATGTTCCGTGCTTCATGGTCAACGACAGAGGCGAGATGATGTCACCTG 237  
QY 501 TTCGCGTGCAGTACTGCTGCGCATCGCCCTTACAGAGGCGGCGCTGCGCTTCA 560  
Db 238 TTCGCTGTCAGTTCACAGCGCTATCGGCCATACAAAGGCGAGTCCGCTCCG 297  
QY 561 TCCGTGAACCTGTCCATCATGAAATTCCTGCTTGAAGCATCTTCAAGAACAGCTG 620  
Db 298 AACGTAACTTTTCATCTCAAGTTCGCGCTGAGAGAACTTCAAGAACTCACTT 357  
QY 621 ACCACCTGCGCCATGGGCGGCGGCAAGGCGGCTCCGACTTCGACCCCAAGGCGAAGAGC 680  
Db 358 ACAACACTCCCAATGGGATGGGCGCAAGGATGCTTCGATTTTCACACCGCGCAAGAGT 417  
QY 681 GACCGGAGGTATGCGCTTTCGCACTGCTTATGACGAGCTGACGCGCCATCAAC 740  
Db 418 GATGGCGAAATCATGAGATTCCTCCAGTATTATGCTCGAACTTTCAGCCCATCGGC 477  
QY 741 TAGTGCAGAGAGTGGCGCGCGGCGACATGGGCTGGGCGCGGCGAGATTGGCTACT 800  
Db 478 GCGAACCAAAATGCTCCAGAGGTGATGCGGTGGTGTGCTGTAAGATGCGCTCAATG 537  
QY 801 TTCGGCCAGTACCAAGCCCATCACAAGAACTACACCGCGCTGTGACCCCGAAGGCGCAG 860  
Db 538 TTCGGCCAGTACCAAGCCCATCACAAGAACTTTCGAGGCGCTCTCACAGGCAAGGCAATC 597  
QY 861 GAGTATGCGCGCTCCGAGATCGCCCGAGGCAACCGGCTACGCGCGCTGCTGTTTGTG 920  
Db 598 TCATTCGGTGGTCACTGGTCCGTCCAGAAAGTACAGGCTACGGTCTTGTCTACTGCTC 657  
QY 921 GAGAACGCTGTAAGAGCAAGGCGGAGAGCTTCAAGGCGCAAGCGCTGCTGCTGCGC 980  
Db 658 ACAGAAATGCTCCGTAATAAGGCGGCAAGATCAAGGCGCAAGGCTGCTGCTGCTGCGC 717  
QY 981 GCGGCGCAAGTGGCGCCGTACTGCGCGGAGCTGCTGTAAGAAAGGCGGCATC 1034  
Db 718 TCCGCGCAAGTCCGACAGTACTGCTGCGAGAGCTATGACGCTCGGCGCAATC 771

RESULT 6 1114 bp DNA linear GSS 05-JUN-2001  
CNS060UN  
LOCUS T3 end of clone AN04A009C04 of library AN04A from strain CLIB 89 of Yarrowia lipolytica, genomic survey sequence.  
DEFINITION  
AL411141  
VERSION AL411141.1 GI:12180271  
KEYWORDS GSS.  
SOURCE Yarrowia lipolytica  
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Dipodascaceae; Yarrowia.



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/clone_lib="Nori Satoh unpublished cDNA library, mature
adult whole animal"

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Query Match	Similarity	Score	DB	Length
Best Local	50.2%	Pred. No. 5.7e-48		
Matches	479;	Conservative	0;	Mismatches 317; Indels 0; Gaps 0
QY	289	TGCGCCAGCTCTGACCGAGATCTTTCATGAAAGACC	CGGAGCAGGAGTTCA	TGCGCAGG
DB	22	TGGACCAAGTGCACAGCTAAAGTACGAAACAGGAGATCCAAACCAACTGATTTTTCAGG		81
QY	349	CGGAGCGGAGGTGGCGCTCCCTCGACGCCCGTGTGAGAAAGGCCCGACGCTGC		408
DB	82	CGGTGAGAGAGGTGCTCATTTTCATTGAAACGGTATTTGATGCGTACCCCAAGTACTTGT		141
QY	409	CCATCTTCACAGCAGATCCGTGAGCCGTGACGCTGATCACCTTCCGCGTGTCTGGCTGG		468
DB	142	CAGTTTTCACAGCAGTGTGCGAGCCAGAAAGGTGTATCAATTCGAGTATCAGTGGCAGG		201
QY	469	ACGAGCCCGGCACTCGAGGTCAACCGCGGCTTCGCGTGAATATCTGTCGCCATCG		528
DB	202	ATGACAAAGGTGACATATCAAAATAAACGAGGCTTCAGAGTCCAGTTTATCAGGCAATTG		261
QY	529	GCCTCTACAAAGGCGGCGCTGCGCTTCCACCCCTCGTAACTGTGCTCATGAAAGTTCC		588
DB	262	GCCGTACAAAGGAGGCTTTGGCTTTCCACCATCGGTCAATCTGCAATCATCAAGTTTC		321
QY	589	TTGCTTTGAGAGATCTTTCAGAAACAGCCTGACCACTTGCCCATGAGGCGCGGCAAG		648
DB	322	TGGGCTTCGACCAATATTTTAAAGACGACTCAACACTTTCATATGGAAGCGCGCAAG		381
QY	649	GGCGCTCCGACTTGGACCCCAAGGCGAGAGGACGGGAGGTATGAGGCTTTCGCCAGT		708
DB	382	GTGGGTGCAATTTTGTATCTCAAGGAGAAACCTGACAGGAAGTTCTCAGTTTTCGACA		441
QY	709	CCTTCATGACCGAGCTGACGCGCCACATCAGCTACGTGACAGACGTGCCCGCGCGACA		768
DB	442	GCTTCATGACGGAAGTTTGTCAAAACATTTGGCCGAGTACGAGCGTCCCGGTGAGATA		501
QY	769	TGCGCGTGGGCGCGCGCGAGATTGGCTACCTTTTCGCGCAGTACAGGCAATCAACAGA		828
DB	502	TTGGGGTCTGGGGGTGAGAAATTTGGCTTCAATGTTTGGACAGTACAAAGTATTAACAACT		561
QY	829	ACTACACCGGCGTGTGACCCCGAAGGCGACAGAGTATGCGCGGCTCCAGATTCGCGCCG		888
DB	562	GCCACCAAGAGTGTGTACCCGGTAAAGAGATGGGGTGTGGGAGAGTTCCGTTATAGCACAG		621
QY	889	AGGCCACCGGCTACGCGCGCGCTGCTGTTTGTGAGAACGTGCTGAGAGACAAAGGCGAGA		948
DB	622	AAGCAACAGGTATTACGGAATTTGTATCGCGCTCGACTTTTGCAATGMAATGTCCGGGAAA		681
QY	949	GCCTCAAGGGGCAAGGCGCTGCCGTGTGTGGGCGGGGCAAGTGGGCCAGTATGCGCGG		1008
DB	682	GCTTTGCGGGGAAAACGCTGACGTTATCTGGTTCTGGGAAAGTGGACAAGTTCCGACAN		741
QY	1009	AGCTGCTGCTGAGAAAGGCGCCATCGTGTGCTGCTGCGACTGCCAGGCGTACGTT		1068
DB	742	ANAAATGCTGGAACCTTGTCGAACGTGCTTACCTTTCACGACGCTGCTGGAATTAATTT		801
QY	1069	ACGAGCCCAAGCGCTT		1084
DB	802	ACNANCCGAAAGGTTT		817

RESULT	8
CV211068/c	
LOCUS	CV211068 943 bp mRNA linear EST 16-SEP-2004
DEFINITION	EST870778 non-normalized t1 cDNA library Trichomonas vaginalis CDNA
ACCESSION	clone TVEB13 3' end, mRNA sequence.
VERSION	CV211068
KEYWORDS	CV211068.1 GI:52158048
	EST.

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	<i>Trichomonas vaginalis</i>					
	<i>Trichomonas vaginalis</i>					
	<i>Eukaryotes: Parabasalidae: Trichomonada; Trichomonadida;</i>					
	<i>Trichomonadidae; Trichomonadinae; Trichomonas.</i>					
	1 (bases 1 to 943)					
	Carlton, J.M., Dyal, S., Johnson, P.J. and Fraser, C.M.					
	The complete genome sequence of the sexually transmitted parasite					
	<i>Trichomonas vaginalis</i>					
	Unpublished (2004)					
	Other ESTs: EST870779					
	Contact: Jane Carlton					
	Parasite Genomics Group					
	The Institute for Genomic Research					
	9712 Medical Center Drive, Rockville, MD 20850, USA					
	Tel: 301-530-9319					
	Fax: 301-838-0208					
	Email: carlton@igf.org					
	Seq primer: polydT 24 base.					
	Location/Qualifiers					
	1..943					

ORIGIN

Query Match	13.5%	Score 288.6;	DB 7;	Length 943;
Best Local Similarity	58.2%	Pred. No. 3.3e-47;		
Matches 548; Conservative	0;	Mismatches 384;	Indels 9;	Gaps 2;

OY	690	GTGATGGCCTTCCTCCAGTCCCTTCATATACGAGCTGCAGGCCCAATCAGGTATGTTGAG	749
Db	943	GTCAATGAGATTCTCCAGCTCACTTTATATGCTGAACTTTACGCCCAATCGCGGCAACACA	884
OY	750	GACGTGCCCGCCGGCGCAATCGAGCGGTGGCGCGCGCGAGATTGGCTACCTTTTGGCCAG	809
Db	883	GATGTCCAGCAGGATGATATCGATGTTGGTCTCGTGAATCCGCTCATATGTTCCGCCAG	824
OY	810	TACAAAGCGCATCACCAAGAACTAACCGGCGTGTGACCCCGAAGGGCCAGGATATGGC	869
Db	823	TACAAAGCGCATCAAGAAAGCTTGTGAAGGCGCTCTCACAGGCAAGGGCGATCTATTGGGT	764
OY	870	GGCTCCGAGATCCGCCCCGAGGCCACCGGCTACGCGCGCGTGTGTTGTGGAGAACGTG	929
Db	763	GGCTCACTGGTCCGTCCAGAGACTACAGGCTACAGGCTTTGTCTACTTTCGTACAGAAATG	704
OY	930	CTGAAGCAAGAGGCGAGAGCCTCAAGGGCAAGCGCTGCTGTGTGTGGCGCGGGCAAC	989
Db	703	CTCCGTACTAAGGGCGAAGAGATCAAGGGCAAGGTGCATGTTTCCGGTCCGGGCAAC	644
OY	990	GTGSCCCAGTACTGCGCGGAGCTCTGCTGTGAGAAAGGCGCCATCTGTGTGTGCTGTCC	1049
Db	643	GTCCCAAGTACTCTGCCAGAAAGCTCATGAGACTCGGCGCAATCCCAAGTCTCATGTCTCA	584
OY	1050	GACTCCCAAGGCGTACGTGTACGAGCCCAACCGGCTTCAACGCGCGAGCGAGCTGACAGGCGGTG	1109
Db	583	GACTCCACCGCGCTCTCATCTTCAAGAGTGTATGACAAAGGAGCACTTTGATGTCTGC	524
OY	1110	CAGGACATGAAGAGAAGAACACAGCGCGCCGC-----ATCTCCGATACAAAGAGCGAC	1163
Db	523	ATGCACATCAAGAAAGCTTGCTCTGTACAGAACTCAAGAAAGATTTAGAACTTTCGCCAGAC	464
OY	1164	ACCGCCGTGTATGTGGCGAACCGCGCGAAGC---TTGGAGACTGGACTGCGCAGGTGGAC	1220



Db 463 CTCAGGGCTACGATGATCATGATGCAATCTCTGGGCTTGCGAAGTTCATGCGAT 404  
Qy 1221 ATTCGCTTCCCTGCGCACCGAAGATTCATGAGCAGACGCGGAGCTGTGATC 1280  
Db 403 ATGGCTCTTCCATGCTGACAGAACGAAATTCCTCCAGACGATTCATCATGATC 344  
Qy 1281 AAGCAGGCTGCGATGATGATGAGGCGCGCAATGCTCTCCACCAAGAGGCCATC 1340  
Db 343 AAGAACGGCGTCAAGCTCTGCGAAGAGTGTCTACATGCAATCAAAAGAGCAATC 284  
Qy 1341 CACAGTCAACAGAGCGCGCATCATCTACTGCTCCCGGCAAGCGCGCAAGCGCGGC 1400  
Db 283 GAGCTCTCATGAGAGAAATCTACTACGCGCCAGCGCAAGCGCCGATGCT 224  
Qy 1401 GTGGCGGTGAGGCGCTGGAATGACCGAAGCCGATGAGCTGTAATGATCGCGAG 1460  
Db 223 GTTCTGTCTCAGGCTGCGAATGACAGAACGCGCTGCGATGATGATCAG 164  
Qy 1461 GAGGTCGCGAAGAGCTGAGCGCATCATGAGACATCTAGACTCCGCCATGAGGCG 1520  
Db 163 AAGGTGCAAGAAAGCTCAAGGAATCATGCAACAATCTTGAAGCGGCCCATTTCTGC 104  
Qy 1521 TCCCGACATACATGTTGACTGCTGCGCGCGCAATCGCGGCTTCAACCAAGGTG 1580  
Db 103 AGTGAGCAGTATGCTTCCACTTACAAAGGCTGCAACTTGGCGGCTTCAAGGCTT 44  
Qy 1581 GCTATGCGCTCAAGGCGCGCTGTTTAAGTGCCTCA 1621  
Db 43 GCCGATGCTATGCTTGCCTACGCGCTGCTAAGCTACGCA 3

RESULT 9  
LOCUS AU186881 540 bp mRNA linear EST 14-OCT-2003  
DEFINITION AU186881 Porphyra yezoensis TU-1 sporophytes Porphyra yezoensis  
cDNA clone PF005C01\_r 5', mRNA sequence.  
ACCESSION AU186881  
VERSION AU186881.1 GI:31919960  
KEYWORDS EST.  
SOURCE Porphyra yezoensis  
ORGANISM Porphyra yezoensis  
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;  
Porphyra.  
REFERENCE 1 (bases 1 to 540)  
Asamizu,E., Nakajima,M., Kitade,Y., Saga,N., Nakamura,Y. and  
Tabata,S.  
COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS  
OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG  
FREQUENCY ANALYSIS  
JOURNAL J. Phycol. 39 (5), 923-930 (2003)  
COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yaku 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
FEATURES  
Source location/Qualifiers  
1..540  
/organism="Porphyra yezoensis"  
/mol\_type="mRNA"  
/strain="TU-1"  
/db\_xref="taxon:2788"  
/clone="PF005C01\_r"  
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/clone\_lib="Porphyra yezoensis TU-1 sporophytes"

ORIGIN  
Query Match 13.2% Score 282.8; DB 1; Length 540;  
Best Local Similarity 70.6%; Pred. No. 4.6e-46;  
Matches 377; Conservative 0; Mismatches 157; Indels 0; Gaps 0;  
Qy 468 GACGACGCGGCAACCTGACAGTCAACCGCGCTTCCCGTGCAGTACTCGTCCGCCATC 527  
Db 5 GATGACGCGGCGGAGCTGCAAGTCAACCGCGCTTCCCGTGCAGTACTCGGATTT 64

Qy 528 GGCCCTTCAAGGGGCGCTGCGCTTCACACCCCTCCGTAACCTGTCCATCATGAAGTTC 587  
Db 65 GGCCCTTCAAGGGGCGGCTTGTCTTCAACCTTACCGTAACCTTCCATCTCAAGTTC 124  
Qy 588 CTTCCTTTAGCAGATCTTCAAGACAGCTGACCAACCTTCCCATAGGCGGCGCAAG 647  
Db 125 CTTCGACGAGGAGGAGTGTGAAGACCGCGTGAAGCTGTGCGGTTGGGCGGCGCAAG 184  
Qy 648 GCGGCTTCCGACTTTCGACCCCAAGGCAAGGCAAGCGGAGGTGATGCTTTCGAG 707  
Db 185 GCGGAGTCTGATTTCAACCTTCAAGGCGCTTCCAGCGGAGGAGGTGCTTTCGAG 244  
Qy 708 TCTTTCATGACCGAGCTGACGCGGCGCATATGACTACGTGACGAGAGCGTCCCGCGGAGAC 767  
Db 245 TCTTTCATGAGGTGCTTGTGCTGCGCACATGCTTCCACACGAGATGTCGCGGAGTAC 304  
Qy 768 ATTCGCGTGGCGCGCGCGAGATTGCTACTTTCGCGCAGTACCAAGCGCATCACCAAG 827  
Db 305 ATTCGAGGTGCTCGGACCGGAGATTGCTACTTGTGGCGGTACCAAGCGGTCACCAAC 364  
Qy 828 AACTACACCGCGCTGCTGACCCCGAAGGCCAGAGATGAGCGGCTTCGAGATTCGCCCC 887  
Db 365 CGCTTTAGGGGCACTCTACGCGGCAAGGCTCTACGTTTGGGAGGCTCCCTCATTCGCCCT 424  
Qy 888 GAGGCCACCGGCTACGCGCGCGCTGCTTGTGTGAGAACGCTGAGAGCAAGGCGGAG 947  
Db 425 GAGTGCACAGGATGAGGCTGTGATGTTGTGTGAGATGCTCAAGGCTCAAGGCGGAT 484  
Qy 948 AGCTCAAGGGCAAGCGCTGCTGTGCTGCGCGCAAGTGGCCAGTAC 1001  
Db 485 ACGCTGAAAGGCAAGGTGTGTGATCTTCGCGAGTGGCAAGTGCCTCCAGTAC 538

RESULT 10  
LOCUS CL693787 820 bp DNA linear GSS 10-JUN-2004  
DEFINITION PR10162C\_B08\_2 - PR10162C\_BR (820) Mixed stage fosmid library of P.  
pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
ACCESSION CL693787  
VERSION CL693787.1 GI:50215695  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
REFERENCE 1 (bases 1 to 820)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
Appads: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
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/db\_xref="taxon:54126"  
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var. California"  
/note="Vector: pBfos-5 Fosmid vector"

ORIGIN

Query Match 13.1%; Score 281; DB 9; Length 820;  
Best Local Similarity 62.5%; Pred. No. 1.1e-45;  
Matches 437; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

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QY 402 CTGCTGCCCATCTTCAAGCAGATCGTTGAGCTGAGCGCGTGAACCTTCCGGCTGCC 461
DB 91 CAGATGTCATTAATGAGCGCTCTGTTGAACCGAGCGCGTGAACGATTTCCGGTGA 150
QY 462 TGGCTGAGACGACGCGGCAACCTGACAGTCAACCGCGCTTCCCGCTGACGATCTGCC 521
DB 151 TGGGTTGATGATCGCAACAGATACAGTCAACCGTGAATGCGCTGACGATTAAGCTCT 210
QY 522 GCCATCGGCGCCCTTCAAGGCGCGCGCTTCCACCCCTCCGTTGAACCTGTCATCATG 581
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DB 271 AATTTCTCGGCTTTGAACAAACCTTCAAAATGCGCTGATCCCTGATCCCTGCGGCGGT 330
QY 642 GGCAGAGGCGGCTCGACTTGAACCCCAAGGCGAAGACGCGGAGTGAATGCGCTTC 701
DB 331 GGTAAAGCGCGACGATTTGATCCGAAGAAAGAAAGCGAAGGTGAAGTGAATGCGTTT 390
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QY 822 ACCAAGAACTACACCGCGTGTGACCCCGAAGGCGCAAGATGAGCGGCTCCGAGATC 881
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DB 751 ACTGTAGTGAATGAAGCGGATTCACGAAGAAAGCACTG 789
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RESULT 11  
LOCUS CF839891 638 bp mRNA linear EST 30-OCT-2003  
DEFINITION pshB004xP07f USDA-IRAFS:Expression of Phytophthora sojae genes during infection and propagation\_sHB Phytophthora sojae cDNA clone SHB004F07 5, mRNA sequence.

ACCESSION CF839891  
VERSION CF839891  
KEYWORDS EST.

SOURCE Phytophthora sojae

ORGANISM Phytophthora sojae  
Phytophthora sojae  
Eukaryota; Stramenopiles; Oomycetes; Pythiales; Pythiaceae;

REFERENCE 1 (bases 1 to 638)

AUTHORS Tyler B. Not Published  
JOURNAL Unpublished (2003)

COMMENT Contact: Tyler B  
Tyler lab

VBI  
1880 Pratt Dr., Blackeburg, VA 24061, USA  
Tel: 540-231-7318  
Email: bmtyle@vt.edu

PCR Primers  
FORWARD: BK reverse primer  
BACKWARD: BK reverse primer  
Plate: 004 row: F column: 07  
Seq primer: BK reverse primer  
High quality sequence stop: 638.

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#### ORIGIN

Query Match 12.8%; Score 274.6; DB 7; Length 638;  
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Matches 426; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

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QY 380 CGTGTGAGAGCGCGCCGAGCTGCTGCCATCTTCAAGCAGATGTTGAGCTTGAAGC 439
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QY 440 CGATACCTTCCGCGTGTCTGCTGAGAGCGCGCGCACTGAGGTCAACCGCG 499
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DB 129 CTTCCGCGTCACTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 188
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DB 189 GGAAGACACCGACGCGCATCCGCAAGTCTGCGCTTCAAGCAGATCTTCCGCAACGCGCT 248
QY 620 GACCACTTCCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 679
DB 249 GCGCGCGCGTAC--GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305
QY 680 CGAAGCGAGGTGATGCTTTCGCGAGTCTTCAATGACCGAGCTGCGAGCGCGCATCAG 739
DB 306 CGAAGCGAGGTGATGCTTTCGCGAGTCTTCAATGACCGAGCTGCGAGCGCGCATCAG 365
QY 740 CTACGTGAGAGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 799
DB 366 CCGGCAACGAGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 425
QY 800 TTTCCGCGATTAAGGCGATCAACGAAGTCAACCGCGGTGCTGACCCCGAAGGCGCA 859
DB 426 GTTCCGCGATTAAGGCGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 479
QY 860 GAGATAGCGCGCTCCGAGATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 919
DB 480 TCTGAGTGAAGCGCGCTTACACATCAACCGCGAGTCAAGGCGTGAAGCGCGCGCGCG 539
QY 920 GGAAGAGTCTGAAGCAAGGCGAGAGCTTCAAGGCGAGCGCTGCTGCTGCTGCTGCTG 979
DB 540 CAACCGCATCTGAGAGCGCGCGAGAGCGTCAAGGCGAAGCGCTGCTGCTGCTGCTGCTG 599
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RESULT 12  
 LOCUS BM436105 727 bp mRNA linear EST 03-JUN-2004  
 DEFINITION BM436105 Nori Satoh unpublished cDNA library, juvenile whole animal  
 Ciona intestinalis cDNA clone cijv03107 5', mRNA sequence.  
 ACCESSION BM436105  
 VERSION BM436105.1 GI:48134395  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Ciona.  
 REFERENCE 1 (bases 1 to 727)  
 AUTHORS Satou,Y., Nakayama,A., Shin-i,T., Kohara,Y. and Satoh,N.  
 TITLE Expressed genes in Ciona intestinalis (2004b)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Nori Satoh  
 Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081  
 Fax: 81-75-705-1113  
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

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ORIGIN  
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 Best Local Similarity 61.2%; Pred. No. 8.1e-44;  
 Matches 436; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

289 TGCAGCAGCTGCTGACCGAGATCTTCATGAAGACCCGAGCAGCAGAGTTGATGACAG 348  
 12 TGGAGAGAGTCAAGCTAAAGTACGAGACGAGGATCCAAACCAATGATTTTGACAG 71  
 349 CGGTGCGGAGGTGCGCTCTCCCTGACGCCGTGTTGAGAAGCGCCCGAGCTGCTGC 408  
 72 CGGTGAGAGAGGTGCTCATTTGATGAACCGTTATTCGATCGTACCCCAAGTACTTGT 131  
 409 CCATCTTCAACGAGATCGTTGAGCGCTGAGCGGTGATCACTTCGCGCTGCTGCTG 468  
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 192 ATGACAGAGGTGACATACAAATTAACCGCGCTTCAGAGTCCAGTTAATCAGGCGCATG 251  
 529 GCCCTTACAGAGCGCGCTGCGCTTCAACCCCTCGTAACCTGTCTCATGAAGTTCC 588  
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 372 GTGGGTGATTTTGTATCAAAAGGAAAACTGACAGGAAAGTTTCAAGTTTGGCGCA 431  
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 DB 552 GCCACCAAGAGGTGCTGACCGGTAAAGATGGGCGGTGGGAGTTTCGCTTATGACCCAN 611  
 QY 889 AGGCGACCGGTAGCGGCGCGTGTGTTGTGAGAAAGTGTGAGGACAGAGGCGCGA 948  
 DB 612 AAGCAACAGGTTAGCGGTGTGTGACCGCGCTGCACTTGCATTAAGATGTCGAAANA 671  
 QY 949 GCTTCAAGGCGAAGCGCTGCGTGTGCTGCGCGCGCGCAAGTGGCCAGTAC 1001  
 DB 672 GCTTCCGCGGAAAAACGTAACGTTATCTGTGTTCTGGGAACGTGCAACATTC 724

RESULT 13  
 LOCUS BM438709 694 bp mRNA linear EST 03-JUN-2004  
 DEFINITION BM438709 Nori Satoh unpublished cDNA library, juvenile whole animal  
 Ciona intestinalis cDNA clone cijv403b07 5', mRNA sequence.  
 ACCESSION BM438709  
 VERSION BM438709.1 GI:48137422  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Ciona.  
 REFERENCE 1 (bases 1 to 694)  
 AUTHORS Satou,Y., Nakayama,A., Shin-i,T., Kohara,Y. and Satoh,N.  
 TITLE Expressed genes in Ciona intestinalis (2004b)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Nori Satoh  
 Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081  
 Fax: 81-75-705-1113  
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

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 Best Local Similarity 62.0%; Pred. No. 1.7e-43;  
 Matches 423; Conservative 0; Mismatches 259; Indels 0; Gaps 0;

318 AAGACCCGAGCAGCAGAGTTATGACGCGGTGCGGAGGTGCGGCTTCCCTGAG 377  
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 QY 378 CCCGTGTTGAGAAAGCGCGAGCTGCGCCATCTTCAAGCAGATGTTGAGCCTGAG 437  
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 QY 438 GCGGTGATCACTTCCGCGTGTCTGCTGAGACGCGCGCAACTGACAGTCAACCGC 497  
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Db 612 CTCACCTTTGGAGTGAAGATGTGCGGAAAGCCTTGGCGGAAACGTTGACGTTATCT 671  
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DEFINITION Bm475527 Nori Satoh unpublished cDNA library, mature adult whole animal Ciona intestinalis cDNA clone cima014f19 5', mRNA sequence.  
ACCESSION Bm475527  
VERSION Bm475527.1 GI:48611391  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.  
REFERENCE 1 (bases 1 to 730)  
AUTHORS Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.  
TITLE Expressed genes in Ciona intestinalis (2004)  
JOURNAL Unpublished (2004)  
COMMENT Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.  
FEATURES  
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Best Local Similarity 61.2%; Pred. No. 2.7e-43;  
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Qy 349 CGGTGCGGAGGTGCGCGTCTCCCTGCAAGCCCGTGTGAGAAAGCGCCCGAGCTGTGC 408  
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Qy 409 CCACTTTCAAGCAGATGTTGAGCTTGAAGCGGTGATCACTTCCGCGTCTCTGCTGG 468  
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Qy 469 ACAGACCGGCGAACCTGCAGSTCAACCGGCGTTCGCGCGTGAAGTACTCGCCGCAATG 528  
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Db 382 GTGGGTGCGATTTTGATCCAAAGGAAAACTGACAGCGAAGTTCTCAGGTTTGGCCAGA 441  
Qy 709 CTTTATGACCGAGCTGCAAGCCCACTCACTACGTACGTGACAGAGTCCCGCGCGAGCA 768  
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Db 562 GCGACCAAGAGTGTGACCGGTAAAGATGGGGTGGGAGGTTGCTTATACAGACAG 621  
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RESULT 15  
LOCUS AUI96696 527 bp mRNA linear EST 15-OCT-2003  
DEFINITION AUI96696 Porphyra yezoensis TU-1 sporophytes Porphyra yezoensis cDNA clone PFL093d06\_1 5', mRNA sequence.  
ACCESSION AUI96696  
VERSION AUI96696.1 GI:31939591  
KEYWORDS EST.  
SOURCE Porphyra yezoensis  
ORGANISM Porphyra yezoensis  
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.  
REFERENCE 1 (bases 1 to 527)  
AUTHORS Aasamizu, S., Nakajima, M., Kikade, Y., Saga, N., Nakamura, Y. and Tabata, S.  
TITLE COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS  
JOURNAL J. Phycol. 39 (5), 923-930 (2003)  
COMMENT Contact: Erika Aasamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1537-3, Kisarazu, Chiba 292-0812, Japan  
Email: aasamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.  
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## ORIGIN

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Matches 362; Conservative 0; Mismatches 160; Indels 0; Gaps 0;  
  
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Qy      440 CGTGATCACTTCCGCGTGTCTGTGAGACGACGCGGCAACTGCAAGTCAACCGCGG 499  
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Qy      860 GGAATATGCGCGCTTCCGAGATCCGCGCCGAGGCCACCGGCTA 901  
Db      486 TACGTTTGGGGGCTCCCTCATTCGCTGAGTGAAGAGGTA 527
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2005, 18:21:52 ; Search time 164 Seconds  
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1240.463 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2105692

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2720	100.0	526	5	AAU98950 NADP-gluc
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4	2621	96.4	512	2	AAW15408 NADP-spec
5	2621	96.4	512	5	AAU98951 NADP-gluc
6	2621	96.4	512	8	ADQ36709 NADP-spec
7	2508	92.2	487	5	AAU98954 Mature NA
8	2508	92.2	487	8	ADQ36729 Mature NA
9	2500	91.9	487	2	AAW15411 NADP-spec
10	2465	90.6	476	2	AAW15412 NADP-spec
11	2465	90.6	476	5	AAU98955 Mature NA
12	2465	90.6	476	8	ADQ36731 Mature NA
13	1309	48.1	445	6	ABU38763 Protein e
14	1309	48.1	450	7	ABO71900 Pseudomon
15	1300.5	47.8	444	8	ADP08330 Neisseria
16	1297.5	47.7	444	6	ABP77942 N. gonorr
17	1297.5	47.7	444	6	ABU37205 Protease
18	1294.5	47.6	444	6	AAU72986 Neisseria
19	1294.5	47.6	444	6	ABU38117 Protein e
20	1287.5	47.3	449	6	ABU39614 Protein e
21	1281	47.1	445	8	ADQ36731 Bacterial
22	1259	46.3	454	8	ADN27186 Bacterial
23	1257.5	46.2	462	6	ABU17276 Protein e
24	1257.5	46.2	467	6	ADQ34438 Acinetoba
25	1250.5	46.0	448	5	ABP65630 Bifidoba

26	1239.5	45.6	448	6	ABU29386	Abu29386 Protein e
27	1239.5	45.6	448	8	ADH97147	Adh97147 E. faecal
28	1239	45.6	449	5	AAU91467	AAU91467 Haemophil
29	1238	45.5	449	4	AAH88536	AAH88536 Haemophil
30	1238	45.5	449	6	ABU30172	ABU30172 Protein e
31	1236.5	45.5	449	5	ABP28423	ABP28423 Streptoco
32	1234.5	45.4	448	7	ADH85999	Adh85999 Enterococ
33	1230.5	45.2	449	6	ABU44405	ABU44405 Protein e
34	1230	45.2	449	6	ABU38946	ABU38946 Protein e
35	1221	44.9	448	8	ADK47974	ADK47974 Streptoco
36	1214	44.6	448	6	ABU46100	ABU46100 Protein e
37	1212	44.6	448	6	ABU01740	ABU01740 S. pneumo
38	1211.5	44.5	448	8	ADH97149	Adh97149 E. faecal
39	1210.5	44.5	458	8	ADS28251	ADS28251 Bacterial
40	1207.5	44.4	464	6	ABU23354	ABU23354 Protein e
41	1205.5	44.3	424	8	ADN17964	ADN17964 Bacterial
42	1205.5	44.3	444	6	ABU20518	ABU20518 Protein e
43	1204	44.3	447	2	AAW08092	AAW08092 Glutamina
44	1201	44.2	447	2	AAW60830	AAW60830 E. coli g
45	1201	44.2	447	6	ABU15360	ABU15360 Protein e

## ALIGNMENTS

AAW15407	standard; protein; 526 AA.
AAW15407;	
17-OCT-2003	(revised)
10-JUL-1997	(first entry)
NADP-specific glutamate dehydrogenase alpha-subunit precursor.	
Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;	
chloroplast; transgenic plant.	
Chlorella sorokiniana; strain UTEX 1230.	
MO9712983-A1.	
10-APR-1997.	
03-OCT-1996;	96WO-US015921.
06-OCT-1995;	95US-00541033.
(UTFL ) UNIV FLORIDA.	
Schmidt RR, Miller P;	
WPI; 1997-226226/20.	
N-PSDB; AAT64529, AAT64542.	
DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism plant cells.	
Claim 1; Page 25-27; 61pp; English.	
2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha and beta subunits (see also AAW15411-12) that comprise the active NADP-GDH hexameric isoenzymes. The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30, AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta	

CC subunits can be expressed that have higher aminating/deaminating activity  
CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.  
CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 526 AA;

Query Match 100.0%; Score 2720; DB 2; Length 526;  
Best Local Similarity 100.0%; Pred. No. 1.3e-250;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVAAPLAPRCLAPWPCAWRSARVDRAKAVSLBEQISAMDATTTGDFTA 60  
DB 1 MOTALVAKPIVAAPLAPRCLAPWPCAWRSARVDRAKAVSLBEQISAMDATTTGDFTA 60  
QY 61 LOKAVKOMATKATGEGVLHGIKNPDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 120  
DB 61 LOKAVKOMATKATGEGVLHGIKNPDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 120  
QY 121 RPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKGLRFPHSVNL 180  
DB 121 RPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKGLRFPHSVNL 180  
QY 181 SIMKFLAFEQIFKNSLITLPMGGGKGSDFDPKGSDAEVRFCQSFMTLQRIHSYVD 240  
DB 181 SIMKFLAFEQIFKNSLITLPMGGGKGSDFDPKGSDAEVRFCQSFMTLQRIHSYVD 240  
QY 241 VPAGDIGVAREIGLFGQYKRIITKNYTGVLTPKGOEYGSSEIRPEATGGAVALFVENVL 300  
DB 241 VPAGDIGVAREIGLFGQYKRIITKNYTGVLTPKGOEYGSSEIRPEATGGAVALFVENVL 300  
QY 301 KDKGESLKGKRCIVSGAGNVAQYCAELLEKGAIIVLSLSDQGYVEBNGFTREQLQAVQ 360  
DB 301 KDKGESLKGKRCIVSGAGNVAQYCAELLEKGAIIVLSLSDQGYVEBNGFTREQLQAVQ 360  
QY 361 DMKKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAFPCATONEIDEHDAELLKHGC 420  
DB 361 DMKKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAFPCATONEIDEHDAELLKHGC 420  
QY 421 QYVEGAMPSSTNEAIHKYNKAGIICPGKANAAGVAVSGLEMTONRMSLNTREVRD 480  
DB 421 QYVEGAMPSSTNEAIHKYNKAGIICPGKANAAGVAVSGLEMTONRMSLNTREVRD 480  
QY 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANAGFTKVADAVAKQAV 526  
DB 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANAGFTKVADAVAKQAV 526

RESULT 2  
AAU98950 standard; protein; 526 AA.

AC AAU98950;  
DT 24-SEP-2002 (first entry)  
DE NADP-glutamate dehydrogenase alpha subunit.  
XX NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;  
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;  
KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.  
OS Chlorella sorokiniana.  
FN US2002062495-A1.  
PD 23-MAY-2002.  
PE 01-MAY-1998; 98US-00070844.  
PR 01-MAY-1998; 98US-00070844.  
PA (SCHMIDT R R.  
PA (MILLER P.

XX Schmidt RR, Miller P;  
XX WPI; 2002-499691/53.  
DR N-PSDB; ABK51007.  
XX

PT Transforming a plant with a polynucleotide encoding a polypeptide with  
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen  
PT metabolism useful to increase yield and ammonium and osmotic stress  
PT tolerance.

XX Claim 6; Page 13-15; 35pp; English.

CC The invention relates to a method of modulating nitrogen metabolism in  
CC plant cells, comprising transforming a plant cell with a polynucleotide  
CC encoding a polypeptide having glutamate dehydrogenase activity, and  
CC culturing the cell to produce descendant cells which express the  
CC polypeptide. The method is used to provide plants with increased yield,  
CC improved ammonium assimilation properties, increased tolerance to ammonia  
CC toxicity, improved osmotic stress tolerance and improved composition. The  
CC present sequence represents the amino acid sequence of Chlorella  
CC sorokiniana NADP-glutamate dehydrogenase alpha subunit, used in the  
CC method of the invention  
XX  
SQ Sequence 526 AA;

Query Match 100.0%; Score 2720; DB 5; Length 526;  
Best Local Similarity 100.0%; Pred. No. 1.3e-250;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVAAPLAPRCLAPWPCAWRSARVDRAKAVSLBEQISAMDATTTGDFTA 60  
DB 1 MOTALVAKPIVAAPLAPRCLAPWPCAWRSARVDRAKAVSLBEQISAMDATTTGDFTA 60  
QY 61 LOKAVKOMATKATGEGVLHGIKNPDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 120  
DB 61 LOKAVKOMATKATGEGVLHGIKNPDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 120  
QY 121 RPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKGLRFPHSVNL 180  
DB 121 RPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVOYSSAIGPYKGLRFPHSVNL 180  
QY 181 SIMKFLAFEQIFKNSLITLPMGGGKGSDFDPKGSDAEVRFCQSFMTLQRIHSYVD 240  
DB 181 SIMKFLAFEQIFKNSLITLPMGGGKGSDFDPKGSDAEVRFCQSFMTLQRIHSYVD 240  
QY 241 VPAGDIGVAREIGLFGQYKRIITKNYTGVLTPKGOEYGSSEIRPEATGGAVALFVENVL 300  
DB 241 VPAGDIGVAREIGLFGQYKRIITKNYTGVLTPKGOEYGSSEIRPEATGGAVALFVENVL 300  
QY 301 KDKGESLKGKRCIVSGAGNVAQYCAELLEKGAIIVLSLSDQGYVEBNGFTREQLQAVQ 360  
DB 301 KDKGESLKGKRCIVSGAGNVAQYCAELLEKGAIIVLSLSDQGYVEBNGFTREQLQAVQ 360  
QY 361 DMKKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAFPCATONEIDEHDAELLKHGC 420  
DB 361 DMKKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAFPCATONEIDEHDAELLKHGC 420  
QY 421 QYVEGAMPSSTNEAIHKYNKAGIICPGKANAAGVAVSGLEMTONRMSLNTREVRD 480  
DB 421 QYVEGAMPSSTNEAIHKYNKAGIICPGKANAAGVAVSGLEMTONRMSLNTREVRD 480  
QY 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANAGFTKVADAVAKQAV 526  
DB 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANAGFTKVADAVAKQAV 526

RESULT 3  
ADQ36707 standard; protein; 526 AA.  
ADQ36707;  
ADQ36707;

DT 23-SEP-2004 (first entry)  
 XX NADP-specific GDH alpha subunit precursor protein, SEQ ID 2.  
 DE Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;  
 KW alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.  
 XX Chlorella sorokiniana.  
 XX US2004128710-A1.  
 PN 01-JUL-2004.  
 PD 24-JUL-2003; 2003US-00627886.  
 PF 01-MAY-1998; 98US-00070844.  
 PR (SCHMIDT R R.  
 XX (MILLER P.  
 PA Schmidt RR, Miller P;  
 PI WPI; 2004-533134/51.  
 DR N-PSDB; ADQ36706.  
 XX  
 PT Increasing or decreasing nitrogen metabolism in plant cells, for plant  
 PT with increased yield and improved tolerance to ammonia toxicity and  
 PT osmotic stress, by transforming plant cell with nucleic acid having  
 PT glutamate dehydrogenase activity.  
 XX  
 XX Claim 7; SEQ ID NO 2; 36pp; English.  
 PS  
 XX The present invention relates to increasing or decreasing the nitrogen  
 CC metabolism in plant cells by transforming a plant cell with a  
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase  
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,  
 CC ADQ36731), or their fragments, which exhibits GDH activity. The  
 CC polynucleotide is operably linked to a polynucleotide encoding a  
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their  
 CC fragments that exhibit chloroplast transit activity. The method is useful  
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The  
 CC methods, polynucleotides, and polypeptides are useful in producing plant  
 CC with increased yield, and with improved tolerance to ammonia toxicity,  
 CC osmotic stress, and composition of the crop or plant. The present  
 CC sequence is the precursor protein of the alpha subunit of the NADP-  
 CC specific GDH, which is then processed to produce the mature alpha subunit  
 CC of the NADP-specific GDH, used in the method of the invention.  
 CC  
 XX Sequence 526 AA;  
 SQ  
 Query Match 100.0%; Score 2720; DB 8; Length 526;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-250;  
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 VPAGDIGVAREIGLFGQYKRITKNYGVLTLPKQGEVGSSEIRPEATGYAVLFEVNVL 300  
 QY 301 KDKGESLKGRCCLVSGAGNNAQVCAELLEKGALVLSLSQGVYEPNGFTREOLAQVQ 360  
 DB 301 KDKESLKGRCCLVSGAGNNAQVCAELLEKGALVLSLSQGVYEPNGFTREOLAQVQ 360  
 QY 361 DMKKNSARISEVKSPTAVVYVGRKRWELDCQVDIAFCATONEIDEHDAELLIKHCQ 420  
 DB 361 DMKKNSARISEVKSPTAVVYVGRKRWELDCQVDIAFCATONEIDEHDAELLIKHCQ 420  
 QY 421 QYVEGANMPSSTNAIHKYNKAGIICPGKAANAGVAVSGLEMTQNRMSLMTREEVVD 480  
 DB 421 QYVEGANMPSSTNAIHKYNKAGIICPGKAANAGVAVSGLEMTQNRMSLMTREEVVD 480  
 QY 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANVAGFTKVDAYKAQCAV 526  
 DB 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANVAGFTKVDAYKAQCAV 526  
 RESULT 4  
 ID AAM15408 standard; protein; 512 AA.  
 AC AAM15408;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 10-JUL-1997 (first entry)  
 XX  
 DE NADP-specific glutamate dehydrogenase beta-subunit precursor.  
 XX  
 KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;  
 KW chloroplast; transgenic plant.  
 XX  
 OS Chlorella sorokiniana; strain UTEX 1230.  
 XX  
 PN M09712983-A1.  
 PD 10-APR-1997.  
 XX  
 XX 03-OCT-1996; 96WO-US015921.  
 PE  
 XX 06-OCT-1995; 95US-00541033.  
 PR  
 PA (UYFL ) UNIV FLORIDA.  
 XX  
 PI Schmidt RR, Miller P;  
 XX  
 DR WPI; 1997-226226/20.  
 DR N-PSDB; AAT64530, AAT64543.  
 XX  
 PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella  
 PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism  
 PT plant cells.  
 XX  
 PS Claim 1; Page 29-32; 61pp; English.  
 XX  
 XX 2 Polypeptides (AAM15407 and AAM15408) respectively comprise the alpha  
 CC (AAM15407) and beta subunit (AAM15408) precursor proteins of an ammonium-  
 CC inducible, chloroplast-localised NADP-specific glutamate dehydrogenase  
 CC (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha  
 CC and beta subunits (see also AAM15411-12) that comprise the active NADP-  
 CC GDH hexameric isoenzymes. The N metabolism of plants can be modulated  
 CC (pref. increasing the assimilation of inorganic N into organic N) by  
 CC transforming them with nucleotide sequences (see also AAT64529-30,  
 CC AAT64547-48) encoding the alpha and/or beta subunits or precursor  
 CC proteins. Such plants show improved properties, e.g. increased crop yield  
 CC and improved stress tolerance. Heterochimers having alpha and beta  
 CC subunits can be expressed that have higher aminating/deaminating activity  
 CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.  
 CC (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 XX Sequence 512 AA;  
 SQ

Query Match 96.4%; Score 2621; DB 2; Length 512;  
Best Local Similarity 97.3%; Pred. No. 3.6e-241;  
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

1 MOTLVAKPIYAAAPLAPRCLAPPCAMVRSARVDRAKAVSLLEQISAMDATTTGDTA 60  
1 MOTLVAKPIYAAAPLAPRCLAPPCAMVRSARVDRAKAVSLLEQISAMDATTTGDTA 46  
1 MOTLVAKPIYAAAPLAPRCLAPPCAMVRSARVDRAKAVSLLEQISAMDATTTGDTA 46

61 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDEPEQOEPMQAVREAVSLQPVFEK 120  
47 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDEPEQOEPMQAVREAVSLQPVFEK 106

121 RPELLPIFKQIVPEPERVITFRVSMWLDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 180  
107 RPELLPIFKQIVPEPERVITFRVSMWLDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 166

181 SIMKFLAFEOIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQOSFMTLQRIHSYVD 240  
167 SIMKFLAFEOIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQOSFMTLQRIHSYVD 226

241 VPAGDIGVAREIGYLFGQYKRTTKNYTGVLTTPKGOEYGSSEIRPEATGYAVLFVENVL 300  
227 VPAGDIGVAREIGYLFGQYKRTTKNYTGVLTTPKGOEYGSSEIRPEATGYAVLFVENVL 286

301 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIIVLSDSQGYVEPNFTREQLQAVQ 360  
287 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIIVLSDSQGYVEPNFTREQLQAVQ 346

361 DMKKKNSARISEKSDTAVYVGRKRPWELDCQVDIAFPQATONEIDEHDAELLIKHGC 420  
347 DMKKKNSARISEKSDTAVYVGRKRPWELDCQVDIAFPQATONEIDEHDAELLIKHGC 406

421 QYVVEGANMPTSTNEAIHKYNKAGIITPCGAANAGVAVSGLEMTONRMSLMTREEVVD 480  
407 QYVVEGANMPTSTNEAIHKYNKAGIITPCGAANAGVAVSGLEMTONRMSLMTREEVVD 466

481 KLERIMKDIYDSAMGSPSRRYNVDLAAGANIAGFTKVADAVKAGAV 526  
467 KLERIMKDIYDSAMGSPSRRYNVDLAAGANIAGFTKVADAVKAGAV 512

RESULT 5  
AAU98951 standard; protein; 512 AA.

AAU98951;  
24-SEP-2002 (first entry)

NADP-glutamate dehydrogenase beta subunit.  
NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;  
nitrogen metabolism; plant; ammonium assimilation; transgenic;  
ammonia toxicity tolerance; osmotic stress tolerance; enzyme.  
Chlorella sorokiniana.  
US200262495-A1.  
23-MAY-2002.  
01-MAY-1998; 98US-00070844.  
01-MAY-1998; 98US-00070844.  
(SCHMIDT R. R.  
(MILLER P.  
Schmidt R. R., Miller P.;  
WPI; 2002-499691/53.  
N-PSDB; ABK51008.

PT Transforming a plant with a polynucleotide encoding a polypeptide with  
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen  
PT metabolism useful to increase yield and ammonium and osmotic stress  
PT tolerance.  
PS Claim 6; Page 17-18; 35pp; English.  
XX  
XX  
CC The invention relates to a method of modulating nitrogen metabolism in  
CC plant cells, comprising transforming a plant cell with a polynucleotide  
CC encoding a polypeptide having glutamate dehydrogenase activity, and  
CC culturing the cell to produce descendant cells which express the  
CC polypeptide. The method is used to provide plants with increased yield,  
CC improved ammonium assimilation properties, increased tolerance to ammonia  
CC toxicity, improved osmotic stress tolerance and improved composition. The  
CC present sequence represents the amino acid sequence of Chlorella  
CC sorokiniana NADP-glutamate dehydrogenase beta subunit, used in the method  
CC of the invention  
XX  
XX  
SQ Sequence 512 AA.

Query Match 96.4%; Score 2621; DB 5; Length 512;  
Best Local Similarity 97.3%; Pred. No. 3.6e-241;  
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

1 MOTLVAKPIYAAAPLAPRCLAPPCAMVRSARVDRAKAVSLLEQISAMDATTTGDTA 60  
1 MOTLVAKPIYAAAPLAPRCLAPPCAMVRSARVDRAKAVSLLEQISAMDATTTGDTA 46  
1 MOTLVAKPIYAAAPLAPRCLAPPCAMVRSARVDRAKAVSLLEQISAMDATTTGDTA 46

61 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDEPEQOEPMQAVREAVSLQPVFEK 120  
47 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDEPEQOEPMQAVREAVSLQPVFEK 106

121 RPELLPIFKQIVPEPERVITFRVSMWLDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 180  
107 RPELLPIFKQIVPEPERVITFRVSMWLDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 166

181 SIMKFLAFEOIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQOSFMTLQRIHSYVD 240  
167 SIMKFLAFEOIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQOSFMTLQRIHSYVD 226

241 VPAGDIGVAREIGYLFGQYKRTTKNYTGVLTTPKGOEYGSSEIRPEATGYAVLFVENVL 300  
227 VPAGDIGVAREIGYLFGQYKRTTKNYTGVLTTPKGOEYGSSEIRPEATGYAVLFVENVL 286

301 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIIVLSDSQGYVEPNFTREQLQAVQ 360  
287 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIIVLSDSQGYVEPNFTREQLQAVQ 346

361 DMKKKNSARISEKSDTAVYVGRKRPWELDCQVDIAFPQATONEIDEHDAELLIKHGC 420  
347 DMKKKNSARISEKSDTAVYVGRKRPWELDCQVDIAFPQATONEIDEHDAELLIKHGC 406

421 QYVVEGANMPTSTNEAIHKYNKAGIITPCGAANAGVAVSGLEMTONRMSLMTREEVVD 480  
407 QYVVEGANMPTSTNEAIHKYNKAGIITPCGAANAGVAVSGLEMTONRMSLMTREEVVD 466

481 KLERIMKDIYDSAMGSPSRRYNVDLAAGANIAGFTKVADAVKAGAV 526  
467 KLERIMKDIYDSAMGSPSRRYNVDLAAGANIAGFTKVADAVKAGAV 512

RESULT 6  
ADQ36709 standard; protein; 512 AA.

ADQ36709;  
23-SEP-2004 (first entry)

NADP-specific GDH beta subunit precursor protein, SEQ ID 4.  
Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;  
beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.

XX Chlorella sorokiniana.  
 OS  
 XX US2004128710-A1.  
 PN  
 XX 01-JUL-2004.  
 PD  
 XX 24-JUL-2003; 2003US-00627886.  
 PF  
 XX 01-MAY-1998; 98US-00070844.  
 PR  
 XX (SCHM/) SCHMIDT R R.  
 PA (MILL/) MILLER P.  
 XX  
 PI Schmidt RR, Miller P;  
 XX  
 DR WPI; 2004-533134/51.  
 DR N-PSDB; ADQ36708.  
 XX  
 PT Increasing or decreasing nitrogen metabolism in plant cells, for plant  
 PT with increased yield and improved tolerance to ammonia toxicity and  
 PT osmotic stress, by transforming plant cell with nucleic acid having  
 PT glutamate dehydrogenase activity.  
 PS  
 PS Claim 7; SEQ ID NO 4; 36pp; English.  
 XX  
 CC The present invention relates to increasing or decreasing the nitrogen  
 CC metabolism in plant cells by transforming a plant cell with a  
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase  
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,  
 CC ADQ36731), or their fragments, which exhibits GDH activity. The  
 CC polynucleotide is operably linked to a polynucleotide encoding a  
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their  
 CC fragments that exhibit chloroplast transit activity. The method is useful  
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The  
 CC methods, polynucleotides, and polypeptides are useful in producing plant  
 CC with increased yield, and with improved tolerance to ammonia toxicity,  
 CC osmotic stress, and composition of the crop or plant. The present  
 CC sequence is the precursor protein of the beta subunit of the NADP-  
 CC specific GDH, which is then processed to produce the mature alpha subunit  
 CC of the NADP-specific GDH, used in the method of the invention.  
 CC  
 SO Sequence 512 AA:

Query Match 96.4%; Score 2621; DB:8; Length 512;  
 Best Local Similarity 97.3%; Pred. No. 3.6e-241;  
 Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MGTALVAKPIYAAFLARPRCLAMPWRSARAKDVRAKVSLEBOISAMDATTTGDTA 60  
 DB 1 MGTALVAKPIYAAFLARPRCLAMPWRSARAKDVRAKVSLEBOISAMDATTTGDTA 46  
 QY 61 LQKAVKQMATKAGTEGLVHGIKNPDVROLLEIFMKDPEOEFQAVREVAVSLOPYEEK 120  
 DB 47 LQKAVKQMATKAGTEGLVHGIKNPDVROLLEIFMKDPEOEFQAVREVAVSLOPYEEK 106  
 QY 121 RPELLPIFKQIWEBERVITFRVSWLDAQNLOVNRGFRVQSSAIGPYKGLRPHPSVNL 180  
 DB 107 RPELLPIFKQIWEBERVITFRVSWLDAQNLOVNRGFRVQSSAIGPYKGLRPHPSVNL 166  
 QY 181 SIMKFLAFEOIFKNSLTTLPMGSGKSGDPFKKSDAEVNRFCOSFMTLEQRIHSYQD 240  
 DB 167 SIMKFLAFEOIFKNSLTTLPMGSGKSGDPFKKSDAEVNRFCOSFMTLEQRIHSYQD 226  
 QY 241 VPADIGVAREIGLFGQYRITKNTYGVLTLPKGOEKGSEIRPEATGYAVFVENVL 300  
 DB 227 VPADIGVAREIGLFGQYRITKNTYGVLTLPKGOEKGSEIRPEATGYAVFVENVL 286  
 QY 301 KDKGESLKGKRCCLVSGAGNVAAQYCAELLEKGAIVLSDSQGYVYEBNGFTREQLAVQ 360  
 DB 287 KDKGESLKGKRCCLVSGAGNVAAQYCAELLEKGAIVLSDSQGYVYEBNGFTREQLAVQ 346

QY 361 DMKKKNSARISEYKSDTAAYVVGDRRKWEIDCCVDIAFPCCATONEIDEHDAELLIKKC 420  
 DB 347 DMKKKNSARISEYKSDTAAYVVGDRRKWEIDCCVDIAFPCCATONEIDEHDAELLIKKC 406  
 QY 421 QYVEGANMSTNEAIHKYNKAGIITCPGKAANGVAVSGLENTONRMSINMTREEYRD 480  
 DB 407 QYVEGANMSTNEAIHKYNKAGIITCPGKAANGVAVSGLENTONRMSINMTREEYRD 466  
 QY 481 KLERIMKDIYDSAMGSPRRYVVDLAAGANTAGFTKVADAVYKAGAV 526  
 DB 467 KLERIMKDIYDSAMGSPRRYVVDLAAGANTAGFTKVADAVYKAGAV 512

RESULT 7  
 ID AAU98954 standard; protein; 487 AA.  
 XX AAU98954;  
 AC  
 XX 24-SEP-2002 (first entry)  
 DT  
 XX Mature NADP-glutamate dehydrogenase alpha subunit.  
 DE  
 XX NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;  
 KW nitrogen metabolism; plant; ammonium assimilation; transgenic;  
 KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.  
 XX  
 OS Chlorella sorokiniana.  
 OS US2002062495-A1.  
 PN  
 XX 23-MAY-2002.  
 PD  
 XX 01-MAY-1998; 98US-00070844.  
 PF  
 XX 01-MAY-1998; 98US-00070844.  
 PR  
 XX 01-MAY-1998; 98US-00070844.  
 PA (SCHM/) SCHMIDT R R.  
 PA (MILL/) MILLER P.  
 PI Schmidt RR, Miller P;  
 XX  
 XX WPI; 2002-499691/53.  
 DR N-PSDB; ABK51025.  
 XX  
 PT Transforming a plant with a polynucleotide encoding a polypeptide with  
 PT glutamate dehydrogenase activity provides a plant with modulated nitrogen  
 PT metabolism useful to increase yield and ammonium and osmotic stress  
 PT tolerance.  
 PS  
 PS Claim 7; Page 27-28; 35pp; English.  
 XX  
 CC The invention relates to a method of modulating nitrogen metabolism in  
 CC plant cells, comprising transforming a plant cell with a polynucleotide  
 CC encoding a polypeptide having glutamate dehydrogenase activity, and  
 CC culturing the cell to produce descendant cells which express the  
 CC polypeptide. The method is used to provide plants with increased yield,  
 CC improved ammonium assimilation properties, increased tolerance to ammonia  
 CC toxicity, improved osmotic stress tolerance, and improved composition. The  
 CC present sequence represents the amino acid sequence of Chlorella  
 CC sorokiniana mature NADP-glutamate dehydrogenase alpha subunit, used in  
 CC the method of the invention  
 CC  
 SO Sequence 487 AA:

Query Match 92.2%; Score 2508; DB:5; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-230;  
 Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AVSLEBOISAMDATTTGDTALQKAVKQMATKAGTEGLVHGIKNPDVROLLEIFMKDPEQ 100  
 DB 2 AVSLEBOISAMDATTTGDTALQKAVKQMATKAGTEGLVHGIKNPDVROLLEIFMKDPEQ 61

QY 101 QEFMOAVREAVASLQPVFEKRPBELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 160  
DB 62 QEFMOAVREAVASLQPVFEKRPBELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 121  
QY 161 YSSAIGPYKGLRPHPSVNLSTIMKFLAFEOIFKNSLTLLPMGGGKGSDDPPKGSDAEV 220  
DB 122 YSSAIGPYKGLRPHPSVNLSTIMKFLAFEOIFKNSLTLLPMGGGKGSDDPPKGSDAEV 181  
QY 221 MRFQSFMTLQRIHSIVQDVPADIGVAREIGYLFQYKRIKNTYGVLTTPKGOEYGG 280  
DB 182 MRFQSFMTLQRIHSIVQDVPADIGVAREIGYLFQYKRIKNTYGVLTTPKGOEYGG 241  
QY 281 SEIRPEATGYCAVLFVENVLKDKGESLKGRKCLVSGAGNAVQYCAELLLEKGAIVLSLD 340  
DB 242 SEIRPEATGYCAVLFVENVLKDKGESLKGRKCLVSGAGNAVQYCAELLLEKGAIVLSLD 301  
QY 341 SOGYVEPNFTREQLQAVODMKKONSARISEKSDTAVYVGGRRPWEIDCQVDIAFP 400  
DB 302 SOGYVEPNFTREQLQAVODMKKONSARISEKSDTAVYVGGRRPWEIDCQVDIAFP 361  
QY 401 CATONEIDEHDAELLIKHGCQYVEGANMPSTNEAIHKYKAGIITCPGKAANAGVAVS 460  
DB 362 CATONEIDEHDAELLIKHGCQYVEGANMPSTNEAIHKYKAGIITCPGKAANAGVAVS 421  
QY 461 GLEWTONRMSLNTREEVDRKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADAV 520  
DB 422 GLEWTONRMSLNTREEVDRKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADAV 481  
QY 521 KAOGAV 526  
DB 482 KAOGAV 487

RESULT 8  
ADQ36729 standard; protein; 487 AA.  
ID ADQ36729  
AC ADQ36729;  
DT 23-SEP-2004 (first entry)  
DE Mature NADP-specific GDH alpha subunit, SEQ ID 24.  
XX Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;  
KM alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.  
XX Chlorella sorokiniana.  
OS  
PN US2004128710-A1.  
XX  
PD 01-JUL-2004.  
XX  
PF 24-JUL-2003; 2003US-00627886.  
XX  
PR 01-MAY-1998; 98US-00070844.  
XX  
PA (SCHMIDT R. R.  
PA (MILLER P.  
XX  
PI Schmidt RR, Miller P;  
XX  
DR WPI; 2004-53134/51.  
DR N-PSDB; ADQ36728.  
XX  
PT Increasing or decreasing nitrogen metabolism in plant cells, for plant  
PT with increased yield and improved tolerance to ammonia toxicity and  
PT osmotic stress, by transforming plant cell with nucleic acid having  
PT glutamate dehydrogenase activity.  
XX  
PS Claim 7; SEQ ID NO 24; 36pp; English.  
XX  
CC The present invention relates to increasing or decreasing the nitrogen  
CC metabolism in plant cells by transforming a plant cell with a

CC polynucleotide encoding a polypeptide having glutamate dehydrogenase  
CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,  
CC ADQ36731), or their fragments, which exhibits GDH activity. The  
CC polynucleotide is operably linked to a polynucleotide encoding a  
CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their  
CC fragments that exhibit chloroplast transit activity. The method is useful  
CC for increasing or decreasing the nitrogen metabolism in plant cells. The  
CC methods, polynucleotides, and polypeptides are useful in producing plant  
CC with increased yield, and with improved tolerance to ammonia toxicity,  
CC osmotic stress, and composition of the crop or plant. The present  
CC sequence is the mature alpha subunit of the NADP-specific GDH used in the  
CC method of the invention.  
XX  
SQ Sequence 487 AA;  
QY 41 AVSLSEQISAMDATTGDFALQKAVKOMATKAGTEGLVHGIKNPDVRLTETIFMKDPEQ 100  
DB 2 AVSLSEQISAMDATTGDFALQKAVKOMATKAGTEGLVHGIKNPDVRLTETIFMKDPEQ 61  
QY 101 QEFMOAVREAVASLQPVFEKRPBELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 160  
DB 62 QEFMOAVREAVASLQPVFEKRPBELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 121  
QY 161 YSSAIGPYKGLRPHPSVNLSTIMKFLAFEOIFKNSLTLLPMGGGKGSDDPPKGSDAEV 220  
DB 122 YSSAIGPYKGLRPHPSVNLSTIMKFLAFEOIFKNSLTLLPMGGGKGSDDPPKGSDAEV 181  
QY 221 MRFQSFMTLQRIHSIVQDVPADIGVAREIGYLFQYKRIKNTYGVLTTPKGOEYGG 280  
DB 182 MRFQSFMTLQRIHSIVQDVPADIGVAREIGYLFQYKRIKNTYGVLTTPKGOEYGG 241  
QY 281 SEIRPEATGYCAVLFVENVLKDKGESLKGRKCLVSGAGNAVQYCAELLLEKGAIVLSLD 340  
DB 242 SEIRPEATGYCAVLFVENVLKDKGESLKGRKCLVSGAGNAVQYCAELLLEKGAIVLSLD 301  
QY 341 SOGYVEPNFTREQLQAVODMKKONSARISEKSDTAVYVGGRRPWEIDCQVDIAFP 400  
DB 302 SOGYVEPNFTREQLQAVODMKKONSARISEKSDTAVYVGGRRPWEIDCQVDIAFP 361  
QY 401 CATONEIDEHDAELLIKHGCQYVEGANMPSTNEAIHKYKAGIITCPGKAANAGVAVS 460  
DB 362 CATONEIDEHDAELLIKHGCQYVEGANMPSTNEAIHKYKAGIITCPGKAANAGVAVS 421  
QY 461 GLEWTONRMSLNTREEVDRKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADAV 520  
DB 422 GLEWTONRMSLNTREEVDRKLERIMKDIYDSAMGPSRRYVNDLAAGANTAGFTKVADAV 481  
QY 521 KAOGAV 526  
DB 482 KAOGAV 487

RESULT 9  
AAW15411  
ID AAW15411 standard; protein; 487 AA.  
AC AAW15411;  
DT 17-OCT-2003 (revised)  
DT 10-JUL-1997 (first entry)  
DE NADP-specific glutamate dehydrogenase alpha subunit.  
XX Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;  
KM chloroplast; transgenic plant.  
XX  
OS Chlorella sorokiniana; strain UTEX 1230.  
XX



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PN  W09712983-A1.
XX
PD  10-APR-1997.
XX
PF  03-OCT-1996; 96WO-US015921.
XX
PR  06-OCT-1995; 95US-00541033.
XX
PA  (UFL ) UNIV FLORIDA.
XX
PI  Schmidt RR, Miller P;
XX
XX  WPI; 1997-226226/20.
DR  N-PSDB; AAT64547.
XX
PT  DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT  sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
XX  plant cells.
XX
PS  Claim 1; Page 44-46; 61pp; English.
XX
XX  2. Polypeptides (AAW15411 and AAW15412) respectively comprise the mature
CC  alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an
CC  ammonium-inducible, chloroplast-localised hexameric NADP-specific
CC  glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
CC  They are produced by removal of transit peptides from the precursor
CC  proteins (AAW15407-08). The N metabolism of plants can be modulated
CC  (pref. increasing the assimilation of inorganic N into organic N) by
CC  transforming them with nucleotide sequences (see also AAT64529-30,
CC  AAT64547-48) encoding the alpha and/or beta subunits or precursor
CC  proteins. Such plants show improved properties, e.g. increased crop yield
CC  and improved stress tolerance. Heterohexamers having alpha and beta
CC  subunits can be expressed that have higher aminating/deaminating activity
CC  ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
CC  (Updated on 17-OCT-2003 to standardise OS field)
XX
XX  Sequence 487 AA:
SQ
Query Match 91.9%; Score 2500; DB 2; Length 487;
Best Local Similarity 99.8%; Pred. No. 1.2e-229;
Matches 485; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

41 AVSLEEDISAMDTGDFTLAQKAVKQMATKATGEGVHGKIPDVRLLTLEIFMKDEQ 100
DB 2 AVSLEEDISAMDTGDFTLAQKAVKQMATKATGEGVHGKIPDVRLLTLEIFMKDEQ 61
QY 101 QEFMQAVREAVASIQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 160
DB 62 QEFMQAVREAVASIQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 121
QY 161 YSSAIGPYKGGRLRHPSPVNSIMKFLAEQIFKNSLTLLPMGGGKGSDFPKGSDAEV 220
DB 122 YSSAIGPYKGGRLRHPSPVNSIMKFLAEQIFKNSLTLLPMGGGKGSDFPKGSDAEV 181
QY 221 MRFCQSMTELORHHSIVQDVPADIGVAREIGVLEQVYRITKNTYGLTTPGQGEKG 280
DB 182 MRFCQSMTELORHHSIVQDVPADIGVAREIGVLEQVYRITKNTYGLTTPGQGEKG 241
QY 281 SEIRPEATGYAVLFEVENVLKDKGESLKGKCLVSGAGNVAQCAELLLEKGAIVLSTSD 340
DB 242 SEIRPEATGYAVLFEVENVLKDKGESLKGKCLVSGAGNVAQCAELLLEKGAIVLSTSD 301
QY 341 SQGVYVEPNCFTREQLQAVQDMKKKNSARISEYKSDTAIVYVGRRKPEWELDCQVDIAFP 400
DB 302 SQGVYVEPNCFTREQLQAVQDMKKKNSARISEYKSDTAIVYVGRRKPEWELDCQVDIAFP 361
QY 401 CATONEIDEHDAELLIRHGCQVYVVGAMSPSTNEAIHKYNKAGITTCGKKAANGAVAS 460
DB 362 CATONEIDEHDAELLIRHGCQVYVVGAMSPSTNEAIHKYNKAGITTCGKKAANGAVAS 421
QY 461 GLENTQNRMSLNTMTREEVRDLERIMKDIYSAMGSPSRVYVVDLAAGANTIGFTKVDAY 520
DB 422 GLENTQNRMSLNTMTREEVRDLERIMKDIYSAMGSPSRVYVVDLAAGANTIGFTKVDAY 481

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QY 521 KAOGAV 526
DB 482 KAOGAV 487

RESULT 10
AAW15412
ID AAW15412 standard; protein; 476 AA.
XX
XX  AAW15412;
XX
XX  17-OCT-2003 (revised)
DT  10-JUL-1997 (first entry)
XX
XX  NADP-specific glutamate dehydrogenase beta subunit.
DE
XX  Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
XX  chloroplast; transgenic plant.
XX
XX  Chlorella sorokiniana; strain UTEX 1230.
OS
XX
XX  W09712983-A1.
XX
XX  10-APR-1997.
PD
XX  03-OCT-1996; 96WO-US015921.
PF
XX  06-OCT-1995; 95US-00541033.
PR
XX
XX  (UFL ) UNIV FLORIDA.
PA
XX
XX  Schmidt RR, Miller P;
PI
XX
XX  WPI; 1997-226226/20.
DR  N-PSDB; AAT64548.
XX
XX  DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT  sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT  plant cells.
XX
XX  Claim 1; Page 48-50; 61pp; English.
XX
XX  2. Polypeptides (AAW15411 and AAW15412) respectively comprise the mature
CC  alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an
CC  ammonium-inducible, chloroplast-localised hexameric NADP-specific
CC  glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
CC  They are produced by removal of transit peptides from the precursor
CC  proteins (AAW15407-08). The N metabolism of plants can be modulated
CC  (pref. increasing the assimilation of inorganic N into organic N) by
CC  transforming them with nucleotide sequences (see also AAT64529-30,
CC  AAT64547-48) encoding the alpha and/or beta subunits or precursor
CC  proteins. Such plants show improved properties, e.g. increased crop yield
CC  and improved stress tolerance. Heterohexamers having alpha and beta
CC  subunits can be expressed that have higher aminating/deaminating activity
CC  ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
CC  (Updated on 17-OCT-2003 to standardise OS field)
XX
XX  Sequence 476 AA:
SQ
Query Match 90.6%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.7e-226;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

51 MDATTGDFTLAQKAVKQMATKATGEGVHGKIPDVRLLTLEIFMKDEQEFMQAVREV 110
DB 1 MDATTGDFTLAQKAVKQMATKATGEGVHGKIPDVRLLTLEIFMKDEQEFMQAVREV 60
QY 111 AVSLOPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVYSSAIGPYK 170
DB 61 AVSLOPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVYSSAIGPYK 120
QY 171 GLRHPSPVNSIMKFLAEQIFKNSLTLLPMGGGKGSDFPKGSDAEVNRFCQSMTE 230

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Db 121 GLRHPSPVNLSIMKFLAFAQIFKNSLTTLPMGSGKGSDFPKGKSDAEVWRFQSPFTE 180  
Qy 231 LQHHISYVQDVPAGDIGVAREIGYLFQYKRTIKNTGVTLPKQGYGSEIRPEATGY 290  
Db 181 LQHHISYVQDVPAGDIGVAREIGYLFQYKRTIKNTGVTLPKQGYGSEIRPEATGY 240  
Qy 291 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSOGYVEPENG 350  
Db 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSOGYVEPENG 300  
Qy 351 FTREQLQAVODMKKKNSARISEYKSDTAVYVGDRRKPMELDCQVDIAFPATONEIDEH 410  
Db 301 FTREQLQAVODMKKKNSARISEYKSDTAVYVGDRRKPMELDCQVDIAFPATONEIDEH 360  
Qy 411 DAELLIRHGGCOYVEGANMPSTNEAHHKYNKAGIITPCGAANAAGVAVSGLEWTQNRMS 470  
Db 361 DAELLIRHGGCOYVEGANMPSTNEAHHKYNKAGIITPCGAANAAGVAVSGLEWTQNRMS 420  
Qy 471 LNMTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVAADAVAKAGAV 526  
Db 421 LNMTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVAADAVAKAGAV 476

## RESULT 11

AU98955 standard; protein; 476 AA.

AAU98955;

24-SEP-2002 (first entry)

Mature NADP-glutamate dehydrogenase beta subunit.

NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;

nitrogen metabolism; plant; ammonium assimilation; transgenic;

ammonia toxicity tolerance; osmotic stress tolerance; enzyme.

Chlorella sorokiniana.

US2002062495-A1.

23-MAY-2002.

01-MAY-1998; 98US-00070844.

01-MAY-1998; 98US-00070844.

(SCHM/) SCHMIDT R R.

(MILL/) MILLER P.

Schmidt RR, Miller P;

WPI; 2002-499691/53.

N-PSDB; ABR51026.

Transforming a plant with a polynucleotide encoding a polypeptide with

glutamate dehydrogenase activity provides a plant with modulated nitrogen

metabolism useful to increase yield and ammonium and osmotic stress

tolerance.

Claim 7; Page 31-32; 35pp; English.

The invention relates to a method of modulating nitrogen metabolism in

plant cells, comprising transforming a plant cell with a polynucleotide

encoding a polypeptide having glutamate dehydrogenase activity, and

culturing the cell to produce descendant cells which express the

polypeptide. The method is used to provide plants with increased yield,

improved ammonium assimilation properties, increased tolerance to ammonia

toxicity, improved osmotic stress tolerance and improved competition. The

present sequence represents the amino acid sequence of Chlorella

sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the

method of the invention

XX Sequence 476 AA;

Query Match 90.6%; Score 2465; DB 5; Length 476;

Best Local Similarity 100.0%; Pred. No.2.7e-226; Indels 0; Gaps 0;

Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 MDAITTGDFTLQCAVAKOMATKAGTEGLVHGIKNPDVRLQTLTEFMKDPEQOEPMQAVREV 110

Db 1 MDAITTGDFTLQCAVAKOMATKAGTEGLVHGIKNPDVRLQTLTEFMKDPEQOEPMQAVREV 60

Qy 111 AVSLQPVFEKRPPELLPIFKQIVPERVITFRVSWLDAGNLQVNRGRVQSSAIGPYKG 170

Db 61 AVSLQPVFEKRPPELLPIFKQIVPERVITFRVSWLDAGNLQVNRGRVQSSAIGPYKG 120

Qy 171 GLRHPSPVNLSIMKFLAFAQIFKNSLTTLPMGSGKGSDFPKGKSDAEVWRFQSPFTE 230

Db 121 GLRHPSPVNLSIMKFLAFAQIFKNSLTTLPMGSGKGSDFPKGKSDAEVWRFQSPFTE 180

Qy 231 LQHHISYVQDVPAGDIGVAREIGYLFQYKRTIKNTGVTLPKQGYGSEIRPEATGY 290

Db 181 LQHHISYVQDVPAGDIGVAREIGYLFQYKRTIKNTGVTLPKQGYGSEIRPEATGY 240

Qy 291 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSOGYVEPENG 350

Db 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSOGYVEPENG 300

Qy 351 FTREQLQAVODMKKKNSARISEYKSDTAVYVGDRRKPMELDCQVDIAFPATONEIDEH 410

Db 301 FTREQLQAVODMKKKNSARISEYKSDTAVYVGDRRKPMELDCQVDIAFPATONEIDEH 360

Qy 411 DAELLIRHGGCOYVEGANMPSTNEAHHKYNKAGIITPCGAANAAGVAVSGLEWTQNRMS 470

Db 361 DAELLIRHGGCOYVEGANMPSTNEAHHKYNKAGIITPCGAANAAGVAVSGLEWTQNRMS 420

Qy 471 LNMTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVAADAVAKAGAV 526

Db 421 LNMTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVAADAVAKAGAV 476

## RESULT 12

ADQ36731 standard; protein; 476 AA.

ADQ36731;

23-SEP-2004 (first entry)

Mature NADP-specific GDH beta subunit, SEQ ID 26.

Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;

beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.

Chlorella sorokiniana.

US2004128710-A1.

01-JUL-2004.

24-JUL-2003; 2003US-00627886.

01-MAY-1998; 98US-00070844.

(SCHM/) SCHMIDT R R.

(MILL/) MILLER P.

Schmidt RR, Miller P;

WPI; 2004-53134/51.

N-PSDB; ADQ36730.

Increasing or decreasing nitrogen metabolism in plant cells, for plant

with increased yield and improved tolerance to ammonia toxicity and

PT osmotic stress, by transforming plant cell with nucleic acid having  
 PT glutamate dehydrogenase activity.  
 XX  
 PS Claim 7; SEQ ID NO 26; 366p; English.  
 XX  
 CC The present invention relates to increasing or decreasing the nitrogen  
 CC metabolism in plant cells by transforming a plant cell with a  
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase  
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH  
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,  
 CC ADQ36731), or their fragments, which exhibits GDH activity. The  
 CC polynucleotide is operably linked to a polynucleotide encoding a  
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their  
 CC fragments that exhibit chloroplast transit activity. The method is useful  
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The  
 CC methods, polynucleotides, and polypeptides are useful in producing plant  
 CC with increased yield, and with improved tolerance to ammonia toxicity,  
 CC osmotic stress, and composition of the crop or plant. The present  
 CC sequence is the mature beta subunit of the NADP-specific GDH used in the  
 CC method of the invention.  
 CC  
 SQ Sequence 476 AA;  
 Query Match 90.6%; Score 2465; DB 8; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-226;  
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 51 MDATGTFPTLQAKVAKOMATAGTEGLVHGKNDVRLTEIFMKDEQGEQMAVREV 110  
 DB 1 MDATGTFPTLQAKVAKOMATAGTEGLVHGKNDVRLTEIFMKDEQGEQMAVREV 60  
 QY 111 AVSLQPVPEKRELLPFFKQIVPEPRTFFVSWLDAQGNQVNRGRPVQSSAIGPKG 170  
 DB 61 AVSLQPVPEKRELLPFFKQIVPEPRTFFVSWLDAQGNQVNRGRPVQSSAIGPKG 120  
 QY 171 GLRHPSPVNSIMKFLAEQIFKNSLTLLPMGSGKSGSDPPKSKDAEVRFCQSFMT 230  
 DB 121 GLRHPSPVNSIMKFLAEQIFKNSLTLLPMGSGKSGSDPPKSKDAEVRFCQSFMT 180  
 QY 231 LQHRISVQDVPADIGVAREIGYLFQGYRITKNTYGVLTLPKQEGVSGSEIRPEATGY 290  
 DB 181 LQHRISVQDVPADIGVAREIGYLFQGYRITKNTYGVLTLPKQEGVSGSEIRPEATGY 240  
 QY 291 GAVLFVENVLKDKESSLKGRCLVSGAGNVQYCAELLLEGAIVLSLSDSQGYVEPBG 350  
 DB 241 GAVLFVENVLKDKESSLKGRCLVSGAGNVQYCAELLLEGAIVLSLSDSQGYVEPBG 300  
 QY 351 FTREQLAVQDMKKKNSARISEYKSDTAVVYVGRKPMELDCQVDIAFPQATONEIDEH 410  
 DB 301 FTREQLAVQDMKKKNSARISEYKSDTAVVYVGRKPMELDCQVDIAFPQATONEIDEH 360  
 QY 411 DAEILLRHGCGQYVEGANGMPSTNEAIHKYKAGIITCYGKAANGVAVSGLMENTONRMS 470  
 DB 361 DAEILLRHGCGQYVEGANGMPSTNEAIHKYKAGIITCYGKAANGVAVSGLMENTONRMS 420  
 QY 471 LMTREVRDGLGEMIDYISANGSPSRRYVNDLAAGNIGFTKYNADAVAAQNAV 526  
 DB 421 LMTREVRDGLGEMIDYISANGSPSRRYVNDLAAGNIGFTKYNADAVAAQNAV 476

## RESULT 13

ABU38763  
 ID ABU38763 standard; protein, 445 AA.  
 XX  
 AC ABU38763;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DB Protein encoded by prokaryotic essential gene #24290.  
 XX  
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Pseudomonas aeruginosa.

XX  
 PN MO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW,  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA42633.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 66687; 1766p; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 445 AA;  
 Query Match 48.1%; Score 1309; DB 6; Length 445;  
 Best Local Similarity 59.2%; Pred. No. 9.3e-116;  
 Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;  
 QY 86 VROLTEIFMKDPQGEQMAVREAVSLQPVPEKRELLP--IFKQIVPEPRTFFVSW 143  
 DB 5 VDAFLERLKRDPQGEQMAVREAVSLQPVPEKRELLP--IFKQIVPEPRTFFVSW 64  
 QY 144 WLDDAGNLQVNRGRPVQSSAIGPKGGLRHPSPVNSIMKFLAEQIFKNSLTLLPMG 203  
 DB 65 WVDQGRVVRVNRGRPVQSSAIGPKGGLRHPSPVNSIMKFLAEQIFKNSLTLLPMG 124

Qy	204	GKGSFDPDKGSDAWMEFCOSFMTLEORH1SVYQVDPADIDIGAREIGEYLGQYKRI	263
		125	GKGSFDPDKGSDAWMEFCOSFMTLEORH1SVYQVDPADIDIGAREIGEYLGQYKRI
Qy	204	GKGSFDPDKGSDAWMEFCOSFMTLEORH1SVYQVDPADIDIGAREIGEYLGQYKRI	263
		125	GKGSFDPDKGSDAWMEFCOSFMTLEORH1SVYQVDPADIDIGAREIGEYLGQYKRI
Qy	264	TKNYTGVLTPKQGEYGSSEIRPEATQYGAULFVENVLKDKESLKGKRCVLGSAGNAYQ	323
		185	SNQFTSVLTKGKLSYGSGLIRPBANGFCGVVFAQEMLRDRGRDQORVAISGSGNAYQ
Qy	324	CABLLEKGAIVL1SLDSQGVYVEBPNGFIREQLOAVQOMKKONNSARISEKSDTAYVYG	383
		245	AAKRWEMNGKXVLSLDSBEGTLYAABGSLDDEWETIMELKXVNR-GKIRREABFSLQFL
Qy	384	DRKPEWELDQVDIAFPFCATONEIDEHDAELLIKHGCOYVVEGAMPSITNEAIIHKYNAG	443
		304	EGRRPGLGAC-DIALPFCATONELEAEDRRLIANGCVCVAGNMPSITNEAVIDLFEAG
Qy	444	IIRCPKGAANAGVAVSGLEMTQNRMSLWMTTEEVRDYLIERIMKDIYDA-MGSPREYNV	502
		362	ILVAPKASNAGSVAVSGLEMSQNMRLRMSGEVDTLTHIMQSIHACILLYEEBGRV
Qy	503	DLAAGANIAGFTVADAVYAKQAV	526
		422	NYVGANLAGEVYKADAMLAQGV

CC	of Pseudomonas species using biochip technology. Sequences AB067826-
CC	components for diagnosis and/or treatment of P. aeruginosa-caused
CC	infection, and in detection of P. aeruginosa sequences or other sequences
CC	production of P. aeruginosa-derived peptides or polypeptides, as target
CC	including anti-P. aeruginosa drugs, as templates for recombinant
CC	effective antibacterial targets, as targets for antibacterial drugs,
CC	for the ability to bind a P. aeruginosa nucleic acid, as components of
CC	bacterial infection, for evaluating a compound, such as a polypeptide,
CC	prophylaxis and treatment of pathological conditions resulting from a
CC	therapy of pathological conditions, as molecular targets for diagnostics,
CC	polynucleotides encoding them. The sequences are useful in diagnosis and
CC	The invention relates to Pseudomonas aeruginosa polypeptides and the
XX	
PS	Disclosure; SEQ ID NO 20646; 455pp; English.
PT	pathological conditions resulting from bacterial infection.
PR	useful as molecular targets for diagnostics, prophylaxis and treatment of
PT	
XX	
XX	(GENO-) GENOME THERAPEUTICS CORP.
PA	
XX	
XX	Rubenfield MJ, Nolling J, Deloughery C, Bush D;
P1	
DR	WPI; 2003-615309/58.
XX	
XX	N-PSDB; ABD05471.
XX	
XX	18-FEB-1999; 99US-C0252991.
PF	
XX	18-FEB-1998; 98US-0074788P.
PR	27-JUL-1998; 98US-0094190P.
XX	
XX	
XX	
OS	Pseudomonas aeruginosa.
XX	
XX	Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
KW	
DE	Pseudomonas aeruginosa polypeptide #4075.
XX	
DT	29-JUL-2004 (first entry)
AC	AB071900;
XX	
XX	AB071900 standard; protein; 450 AA.
ID	AB071900
RESULT 14	

CC AAO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX  
SQ Sequence 450 AA;

Query Match	48.1%;	Score 1309;	DB 7;	Length 450;
Best Local Similarity	59.2%;	Pred. NO. 9.4e-116;		
Matches 263;	Conservative 55;	Mismatches 120;	Indels 6;	Gaps 4;

Qy	86	VRLTLEIMKDPEDQOEFOQAVREVAVSLQCPVEKRPBLLP--IFKQIVPEKVIFFRS	143
Db	10	VDALFLERLKRDPDQPEFHQAIVEVLRSLWFLFLEAHNYLEAGIIRIIVPERAILFRVP	69
Qy	144	WLDAGNLQVNTGFVRVQYSSAIGPYKGGLRHPSPVNLSIMKFLAFEDIFKNSLTLLPMGG	203
Db	70	WVDQQRVRVNNGVYQWMSAIGPYKGGLRHPSPVNINIGYKFLAFEDVFNKSLTLLPMGG	129
Qy	204	GKGGSPDFDKGSDAEWRFCOSFWTELQRIHSVODVPVPGDIDGVARIEIGYFGQYKRI	263
Db	130	GKGGSPDFDKGSDAEWRFCOSFWSELYRHHVAGDLDPVAGDIDGVARIEIGYFGQYKRL	189
Qy	264	TKNYTVLTPKQOEYGESEIRPEATYGAVLFEVNLKDKESLKGRCCLVSGAGNVAOY	323
Db	190	SNQFTSVLTKGSLTSGSLIRPEATGFCGYFAQEMLKDRGPFQGRVAVISGGNVAQY	249
Qy	324	CAELLLEKAYLVSLSDSQYTYENGGTRRQLOAVQDMKKKNNSAISIRYKDTVAVYG	383
Db	250	AAKRWEMEGKAYISLSDSBGLTYABAGISDBQWEMELMKVNR--GRIRMAEQFSIQPL	308
Qy	384	DREKPEWELCCQVDIAFPQATONEIDEHDAELLKHGCOYVEGANMPSYTEALHRYKNKAG	443
Db	309	EGRRPGLAC--DIALPCATQNEIDAEARRLLANGCYAAEGANMPSITLBAVDLFLEAG	366
Qy	444	IYCPGKANAGGVAVSGLEMTQNMKSLMWTREEVDRKLERIMKDIYDSA--MGDSRRYNY	502
Db	367	IIVAPPKASNAGGVAVSGLEMSQNMRRLRMEGEVDTLHGIMQSIHACILLGEQGRV	426
Qy	503	DLAAGANIAGFTKVDAYKAGAV	526
Db	427	NYKGANIAGFKVADAMLAGV	450

[illegible]

DR WPI: 2004-420615/39.

XX New compositions having outer-membrane vesicles and proteins from  
PT *Neisseria meningitidis*, useful in the field of meningococcal  
PT biochemistry, in particular for preventing and/or treating meningococcal  
PT infections.

PS Claim 9; SEQ ID NO 163; 79pp; English.

XX  
XX  
CC The invention relates to a novel composition comprising outer-membrane  
CC vesicles (OMV) prepared from a first strain of *Neisseria meningitidis* and  
CC 1 or more proteins which are present in OMVs prepared from a second  
CC strain of *N. meningitidis*, but which are not present in OMVs prepared  
CC from the first strain. The composition of the invention demonstrates  
CC antibacterial and anti-inflammatory activities and may be useful in the  
CC field of meningococcal biochemistry, in particular the trafficking and  
CC localisation of meningococcal proteins, as well as in the prevention or  
CC treatment of meningococcal infections, possibly via the production of a  
CC vaccine or gene therapy. The current sequence is that of a *Neisseria*  
CC meningitidis MCS8 outer-membrane vesicle (OMV)-related membrane protein  
CC of the invention.

XX Sequence 444 AA;

Query Match 47.8%; Score 1300.5; DB 8; Length 444;  
Best Local Similarity 57.4%; Pred. No. 66-115;  
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 85 DVRLTLTEIFMKDEQEFMQAVREAVSLQVFEKRELL--PIFKQIVEPERVITFRV 142  
DB 3 DLNLTFLANLKKRNPNQSEPFHQAVEVFWMSLDPLAKNPKYQOSLIERIVEPERVWFRV 62  
QY 143 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRFPSPVNLSTIMKFLAFEOIFKNSLTLLPMG 202  
DB 63 TWODDKQOVQVNRGRFRVQYSSAIGPYKGLRFPSPVNLSTIMKFLAFEOIFKNSLTLLPMG 122  
QY 203 GKGSGSPDFDPKGSADAEVNRFCQSPFTELRHISVYODVPADIGVGAREIGYLFQGYKR 262  
DB 123 GKGSGSPDFDPKGSADAEVNRFCQSPFTELRHISVYODVPADIGVGAREIGYLFQGYKR 182  
QY 263 ITKNYTVGLTPKGOEYGGSEIRPEATGYAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 322  
DB 183 IRNEFSSVLTGKLEWGSGLIRPEATGYAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 242  
QY 323 YCAELLEKGAIVLSDSQGYTER-NGFTREQLQAVQMKKXNSARISEYKSDTAVY 381  
DB 243 YAAEKAIQLGAKVLTVSDSNGFVLPDSCGTEAQLAALIEIKVRRR-RVATYAKEQGLQ 301  
QY 382 VGDRRKPEMLDCCVDIAFPCATONEIDEHDAELLIXGQCVVVEGANNPSTNEAIHKYK 441  
DB 302 YFEKQKPMGV--AAEIALPCATONEIDEHDAELLIXGQCVVVEGANNPSTLGAVEQFIK 359  
QY 442 AGIITYCPKAAAGVAVSGLEMTQNRMSLNTREEVYDKLERIMKDIYDSAMGPSRRY- 500  
DB 360 AGIITYAGKASNAGVATSGLEWSONAIRLSMTREBYDQRLFGIMOSIHESCL----KYG 415  
QY 501 ----NVDLAAGANIAGFTKVAADAVKAAQ 524  
DB 416 KVGDTVYVYNGANIGFVKVADAMLAQG 443

Search completed: July 9, 2005, 18:32:04  
Job time: 174 secs

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## OM protein - protein search, using SW model

Run on: July 9, 2005, 18:26:33 ; Search time 43 Seconds

(without alignments)  
913.149 Million cell updates/sec

Title: US-10-627-886-2

Perfect score: 2720  
Sequence: 1 MOTALVAKPIVAAPLAARPR.....GANIAGFTKVAADAVKAGAV 526

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/6C\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2720	100.0	526	2	US-08-541-033A-2
2	2720	100.0	526	2	US-08-828-451-2
3	2621	96.4	512	2	US-08-541-033A-4
4	2621	96.4	512	2	US-08-828-451-4
5	2508	92.2	487	2	US-08-541-033A-24
6	2508	92.2	487	2	US-08-828-451-24
7	2465	90.6	476	2	US-08-541-033A-26
8	2465	90.6	476	2	US-08-828-451-26
9	1309	48.1	450	4	US-09-252-991A-20646
10	1257.5	46.2	467	4	US-09-328-352-5725
11	1234.5	45.4	448	4	US-09-134-000C-3884
12	1221	44.9	448	4	US-09-583-110-4489
13	1201	44.2	447	2	US-08-886-640-3
14	1201	44.2	447	3	US-08-886-640-3
15	1200	44.1	447	1	US-08-370-193A-11
16	1191	43.8	452	4	US-09-489-039A-7937
17	1177.5	43.3	446	4	US-09-543-681A-6657
18	1177	43.3	447	3	US-08-508-761B-6
19	1147	42.2	461	3	US-09-171-337A-5
20	1147	42.2	461	4	US-09-631-022-5
21	1143	42.0	449	1	US-08-831-753-1
22	1037.5	38.1	454	4	US-09-538-092-767
23	1012	37.2	368	4	US-09-107-433-4041
24	788.5	29.0	298	4	US-09-248-796A-17483
25	552.5	20.3	420	3	US-09-134-001C-3103
26	537.5	19.8	374	4	US-09-710-279-2162
27	537	19.7	509	4	US-09-902-540-11352

28	519	19.1	420	3	US-09-239-303-9	Sequence 9, Appl1
29	482.5	17.7	409	4	US-09-902-540-12638	Sequence 12638, A
30	476.5	17.5	421	3	US-09-239-303-2	Sequence 2, Appl1
31	458.5	16.9	427	4	US-09-328-352-6130	Sequence 6130, Ap
32	441	16.2	432	4	US-09-489-039A-13935	Sequence 13935, A
33	385	14.2	87	2	US-08-461-990B-22	Sequence 22, Appl1
34	368	13.5	87	2	US-08-461-990B-20	Sequence 20, Appl1
35	364.5	13.4	558	4	US-09-538-092-1153	Sequence 1153, Ap
36	357	13.1	87	2	US-08-461-990B-23	Sequence 23, Appl1
37	357	13.1	558	4	US-09-538-092-832	Sequence 832, App
38	357	13.1	575	4	US-09-949-016-7622	Sequence 7622, Ap
39	357	13.1	575	4	US-09-949-016-7623	Sequence 7623, Ap
40	346	12.7	176	4	US-09-248-796A-17482	Sequence 17482, A
41	168	6.2	87	2	US-08-461-990B-21	Sequence 21, Appl1
42	157.5	5.8	366	2	US-08-804-689-2	Sequence 2, Appl1
43	139.5	5.1	356	2	US-08-461-990B-2	Sequence 122, App
44	138	5.1	1092	4	US-09-538-092-122	Sequence 991, App
45	131	4.8	351	4	US-09-198-452A-991	

## ALIGNMENTS

## RESULT 1

US-08-541-033A-2

Sequence 2, Application US/08541033A

Patent No. 5879941

GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

APPLICANT: Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE

NUMBER OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Saliwanchik &amp; Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/541,033A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Whitlock, Ted W.

REGISTRATION NUMBER: 36,965

REFERENCE/DOCKET NUMBER: UP155

TELECOMMUNICATION INFORMATION:

TELEPHONE: (904) 375-8100

TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 526 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-541-033A-2

Query Match

Best Local Similarity 100.0%; Pred. No. 7, 6e-243;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

Db

1 MOTALVAKPIVAAPLAARPRCLAPWPCAWRSARADYRAKAVSLIEQISAMDATGDFTA 60

1 MOTALVAKPIVAAPLAARPRCLAPWPCAWRSARADYRAKAVSLIEQISAMDATGDFTA 60

Qy	6	LOKAVOMATKATGTEGHVGIKNPDRLOLTETPKKDQOOFPMQAVEVNSLOPFEK	120
Db	61	LOQAVOMATKAGTBEUHVHGIKNPDRLOLTETPKKDQOOFPMQAVEVNSLOPFEK	120
Qy	121	RPELLPIFKQIVBERVITFRVSWLDDAGNLQVNGFRVQYSSAIGPYKGLRFPHSVNL	180
Db	121	RPELLPIFKQIVBERVITFRVSWLDDAGNLQVNGFRVQYSSAIGPYKGLRFPHSVNL	180
Qy	181	SIMKPLAFBEOIFKNSLTTLPMGGGKGSPDRKGSDBAENRFQCSFMTLQRIHSYOD	240
Db	181	SIMKPLAFBEOIFKNSLTTLPMGGGKGSPDRKGSDBAENRFQCSFMTLQRIHSYOD	240
Qy	241	VPAAGDIGVAREIGLYLFGQYKRTITKNYTVTLTPKQOEYSGSEIREATGAVLFEVNL	300
Db	241	VPAAGDIGVAREIGLYLFGQYKRTITKNYTVTLTPKQOEYSGSEIREATGAVLFEVNL	300
Qy	301	KDQGESLKGKRCIVSAGVAVOYCAELLLEKAVILSLSDSGYIYEPNGTREBOLQAVQ	360
Db	301	KDQGESLKGKRCIVSAGVAVOYCAELLLEKAVILSLSDSGYIYEPNGTREBOLQAVQ	360
Qy	361	DMKKONNSARISEYKSDTAVVYGGDRKRPPELLCCQVDIAFPQATONEIDEHAAELLIHGC	420
Db	361	DMKKONNSARISEYKSDTAVVYGGDRKRPPELLCCQVDIAFPQATONEIDEHAAELLIHGC	420
Qy	421	QYVEEGANPSTNEALHKYNKAGIYCPGKANAGGVAVSGLEMTQNRMSLNTMREEVRD	480
Db	421	QYVEEGANPSTNEALHKYNKAGIYCPGKANAGGVAVSGLEMTQNRMSLNTMREEVRD	480
Qy	481	KLERIKMDIYDSAMGSRRYNVDLAAGANIAFTVAADVAQAQAV	526
Db	481	KLERIKMDIYDSAMGSRRYNVDLAAGANIAFTVAADVAQAQAV	526

## RESULT 2

US-08-828-451-2  
Sequence 2, Application US/08828451  
Patent No. 5985634  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,451  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whillock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 526 amino acids

```

;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-828-451-2

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Query Match	100.0%;	Score 2720;	DB 2;	Length 526;
Best Local Similarity	100.0%;	Pred. No. 7.6e-243;		
Matches 526;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MQALVAKKI	1	VAAPLAPRCLAPMP	CAMVS	SARKDPAKVS	LEBIS	ISAMD	ITGG	FTA	60						
Dp	1	MQALVAKKI	1	VAAPLAPRCLAPMP	CAMVS	SARKDPAKVS	LEBIS	ISAMD	ITGG	FTA	60						
Qy	61	LOAVNQMA	1	TKAGTEB	LHGKINP	VRULL	LEI	FMKD	PEOE	FMQAVRE	VAVS	LOPFEK	120				
Dp	61	LOAVNQMA	1	TKAGTEB	LHGKINP	VRULL	LEI	FMKD	PEOE	FMQAVRE	VAVS	LOPFEK	120				
Qy	121	REPELPI	1	FQAI	VEPERVIT	FRVSW	LDADGN	QVNR	GFVQVS	SAI	IGYKGL	LFHPSVNL	180				
Dp	121	REPELPI	1	FQAI	VEPERVIT	FRVSW	LDADGN	QVNR	GFVQVS	SAI	IGYKGL	LFHPSVNL	180				
Qy	181	STIKETLAP	1	FOIRFNS	LITTL	PMGGG	GGSGSD	PDPKG	SDAEVNR	FOQSMTEL	ORHIS	SVOD	240				
Dp	181	STIKETLAP	1	FOIRFNS	LITTL	PMGGG	GGSGSD	PDPKG	SDAEVNR	FOQSMTEL	ORHIS	SVOD	240				
Qy	241	VPAQD	1	IGVARE	IGYLF	GOYKR	ITKNY	GYVLT	PKGOE	GGSEIR	EPATG	YGAULF	VEVNYL	300			
Dp	241	VPAQD	1	IGVARE	IGYLF	GOYKR	ITKNY	GYVLT	PKGOE	GGSEIR	EPATG	YGAULF	VEVNYL	300			
Qy	301	KDKESL	1	KGRCLV	SGAGN	VAOY	CALLE	LEKGA	IVLS	DSOGY	VE	PNGTRE	LOAVO	360			
Dp	301	KDKESL	1	KGRCLV	SGAGN	VAOY	CALLE	LEKGA	IVLS	DSOGY	VE	PNGTRE	LOAVO	360			
Qy	361	DMKKNS	1	ARISEY	SDPTAVY	YGD	RKWE	LD	COVD	IAP	CATONE	I	DEHDA	ELLKHGC	420		
Dp	361	DMKKNS	1	ARISEY	SDPTAVY	YGD	RKWE	LD	COVD	IAP	CATONE	I	DEHDA	ELLKHGC	420		
Qy	421	QYVEG	1	ANPSTNEA	I	HKYN	KAGI	I	YCP	GAAN	AGVA	SVSGLE	MTON	RMS	LNT	TRREVRD	480
Dp	421	QYVEG	1	ANPSTNEA	I	HKYN	KAGI	I	YCP	GAAN	AGVA	SVSGLE	MTON	RMS	LNT	TRREVRD	480
Qy	481	KLERIM	1	KD	IYDS	AMG	BSRR	VND	I	LAAG	NI	IGFT	KVAD	VA	YAO	QAV	526
Dp	481	KLERIM	1	KD	IYDS	AMG	BSRR	VND	I	LAAG	NI	IGFT	KVAD	VA	YAO	QAV	526

### RESULT 3

US-08-541-033A-4  
Sequence 4, Application US/08541033A  
Patent No. 5879941  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Salivanchik & Salivanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033A  
FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-541-033A-4

Query Match 96.4%; Score 2621; DB 2; Length 512;  
Best Local Similarity 97.3%; Pred. No. 1,1e-233;  
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTLVAKPIVAAPLAARPCCLAPWPCAWRSARQDVAKAVSLSEBOISAMDATTTGDTA 60  
DB 1 MOTLVAKPIVA-----CAWRSARQDVAKAVSLSEBOISAMDATTTGDTA 46  
QY 61 LQKAVKQMATKAGTEGLVHGINKPVDVRLTEIFMKDPEOEFMOAVREAVVSLQPVREK 120  
DB 47 LQKAVKQMATKAGTEGLVHGINKPVDVRLTEIFMKDPEOEFMOAVREAVVSLQPVREK 106  
QY 121 RPBLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRHPHSVNL 180  
DB 107 RPBLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRHPHSVNL 166  
QY 181 SIMKFLAFEOIFKNSLTLLPMGGSGGSDPDKGSDAEVNRFCOSFTTELQRIHSYQD 240  
DB 167 SIMKFLAFEOIFKNSLTLLPMGGSGGSDPDKGSDAEVNRFCOSFTTELQRIHSYQD 226  
QY 241 VPAGDIGVAREIGYLFQYKRIITKNYTVLTPKQEGYSGEIRPEATGAVLFVENVL 300  
DB 227 VPAGDIGVAREIGYLFQYKRIITKNYTVLTPKQEGYSGEIRPEATGAVLFVENVL 286  
QY 301 KDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGETRQLOAVQ 360  
DB 287 KDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGETRQLOAVQ 346  
QY 361 DMKKKNSARISEKSDTAAYVVGDRRKWEIDCCVDIAFPCATONEIDEHDAELLIRHGC 420  
DB 347 DMKKKNSARISEKSDTAAYVVGDRRKWEIDCCVDIAFPCATONEIDEHDAELLIRHGC 406  
QY 421 QYVEGANMPSSTNEAIHKYNKAGIIPCCKAANAGVAVSGLEMTQNRMSLMTREEVRD 480  
DB 407 QYVEGANMPSSTNEAIHKYNKAGIIPCCKAANAGVAVSGLEMTQNRMSLMTREEVRD 466  
QY 481 KLERIMDIYDSAMGPRRRYVNDLAAGANIAGFTKVADAVAKQAV 526  
DB 467 KLERIMDIYDSAMGPRRRYVNDLAAGANIAGFTKVADAVAKQAV 512

RESULT 4  
US-08-828-451-4  
Sequence 4, Application US/08828451  
Patent No. 5985634  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Saliwanichik & Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA

ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,451  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-828-451-4

Query Match 96.4%; Score 2621; DB 2; Length 512;  
Best Local Similarity 97.3%; Pred. No. 1,1e-233;  
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTLVAKPIVAAPLAARPCCLAPWPCAWRSARQDVAKAVSLSEBOISAMDATTTGDTA 60  
DB 1 MOTLVAKPIVA-----CAWRSARQDVAKAVSLSEBOISAMDATTTGDTA 46  
QY 61 LQKAVKQMATKAGTEGLVHGINKPVDVRLTEIFMKDPEOEFMOAVREAVVSLQPVREK 120  
DB 47 LQKAVKQMATKAGTEGLVHGINKPVDVRLTEIFMKDPEOEFMOAVREAVVSLQPVREK 106  
QY 121 RPBLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRHPHSVNL 180  
DB 107 RPBLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRHPHSVNL 166  
QY 181 SIMKFLAFEOIFKNSLTLLPMGGSGGSDPDKGSDAEVNRFCOSFTTELQRIHSYQD 240  
DB 167 SIMKFLAFEOIFKNSLTLLPMGGSGGSDPDKGSDAEVNRFCOSFTTELQRIHSYQD 226  
QY 241 VPAGDIGVAREIGYLFQYKRIITKNYTVLTPKQEGYSGEIRPEATGAVLFVENVL 300  
DB 227 VPAGDIGVAREIGYLFQYKRIITKNYTVLTPKQEGYSGEIRPEATGAVLFVENVL 286  
QY 301 KDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGETRQLOAVQ 360  
DB 287 KDKGESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGETRQLOAVQ 346  
QY 361 DMKKKNSARISEKSDTAAYVVGDRRKWEIDCCVDIAFPCATONEIDEHDAELLIRHGC 420  
DB 347 DMKKKNSARISEKSDTAAYVVGDRRKWEIDCCVDIAFPCATONEIDEHDAELLIRHGC 406  
QY 421 QYVEGANMPSSTNEAIHKYNKAGIIPCCKAANAGVAVSGLEMTQNRMSLMTREEVRD 480  
DB 407 QYVEGANMPSSTNEAIHKYNKAGIIPCCKAANAGVAVSGLEMTQNRMSLMTREEVRD 466  
QY 481 KLERIMDIYDSAMGPRRRYVNDLAAGANIAGFTKVADAVAKQAV 526  
DB 467 KLERIMDIYDSAMGPRRRYVNDLAAGANIAGFTKVADAVAKQAV 512

RESULT 5  
US-08-541-033A-24  
Sequence 24, Application US/08541033A  
Patent No. 5879941

```
/ GENERAL INFORMATION:
/ APPLICANT: Schmidt, Robert R.
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
/ TITLE OF INVENTION: RELATING TO THE -- AND -SUBUNITS OF GLUTAMATE
/ TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/541,033A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Whitlock, Ted W.
/ REGISTRATION NUMBER: 36,965
/ REFERENCE/DOCKET NUMBER: UP155
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 487 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-541-033A-24
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```
Query Match          92.2%; Score 2508; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No.2.8e-223;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AVSLBEOISAMDATGDTFTALOKAVKOMATKAGTEGLVHGIKNPDVRLTLTEIFMKDPEQ 100
DB 2 AVSLBEOISAMDATGDTFTALOKAVKOMATKAGTEGLVHGIKNPDVRLTLTEIFMKDPEQ 61
QY 101 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 160
DB 62 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 121
QY 161 YSSAIGPYKGLRPHBPNVNSIMKFLAFEOIFKNSLTTLPMGGGSGSDPDKGSDAEV 220
DB 122 YSSAIGPYKGLRPHBPNVNSIMKFLAFEOIFKNSLTTLPMGGGSGSDPDKGSDAEV 181
QY 221 MRFQSFMTLQRIHSYQVDPAGDIGVAREIGYLFQGYKRTIKNTYGVLTTPKGOEYGG 280
DB 182 MRFQSFMTLQRIHSYQVDPAGDIGVAREIGYLFQGYKRTIKNTYGVLTTPKGOEYGG 241
QY 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGNVAQYCAELLLEKGAIVLSLSD 340
DB 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGNVAQYCAELLLEKGAIVLSLSD 301
QY 341 SQGVYVPNGFTTRQLOAVODMKKKNNSARISEYKSPTAVVVGRRRKRWELDCOVDAFP 400
DB 302 SQGVYVPNGFTTRQLOAVODMKKKNNSARISEYKSPTAVVVGRRRKRWELDCOVDAFP 361
QY 401 CATONEIDEHDAELLIKHGCOYVEGANMPESTNEAIHKYNKAGIITYCGKANAAGVAVS 460
DB 362 CATONEIDEHDAELLIKHGCOYVEGANMPESTNEAIHKYNKAGIITYCGKANAAGVAVS 421
QY 461 GLENTQRMKSINMTREEVRLDLERIMKDIYDSAMGSPSRNVNDLAAGANTAGFTTKVADAV 520
DB 422 GLENTQRMKSINMTREEVRLDLERIMKDIYDSAMGSPSRNVNDLAAGANTAGFTTKVADAV 481
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QY 521 KAOGAV 526
DB 482 KAOGAV 487

RESULT 6
US-08-828-451-24
/ Sequence 24, Application US/08828451
/ Patent No. 5985634
/ GENERAL INFORMATION:
/ APPLICANT: Schmidt, Robert R.
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
/ TITLE OF INVENTION: RELATING TO THE -- AND -SUBUNITS OF GLUTAMATE
/ TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/828,451
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/541,033
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Whitlock, Ted W.
/ REGISTRATION NUMBER: 36,965
/ REFERENCE/DOCKET NUMBER: UP155
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 487 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-828-451-24

Query Match          92.2%; Score 2508; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No.2.8e-223;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AVSLBEOISAMDATGDTFTALOKAVKOMATKAGTEGLVHGIKNPDVRLTLTEIFMKDPEQ 100
DB 2 AVSLBEOISAMDATGDTFTALOKAVKOMATKAGTEGLVHGIKNPDVRLTLTEIFMKDPEQ 61
QY 101 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 160
DB 62 QEFMQAVREVAVSLQVPFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 121
QY 161 YSSAIGPYKGLRPHBPNVNSIMKFLAFEOIFKNSLTTLPMGGGSGSDPDKGSDAEV 220
DB 122 YSSAIGPYKGLRPHBPNVNSIMKFLAFEOIFKNSLTTLPMGGGSGSDPDKGSDAEV 181
QY 221 MRFQSFMTLQRIHSYQVDPAGDIGVAREIGYLFQGYKRTIKNTYGVLTTPKGOEYGG 280
DB 182 MRFQSFMTLQRIHSYQVDPAGDIGVAREIGYLFQGYKRTIKNTYGVLTTPKGOEYGG 241
QY 281 SEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGNVAQYCAELLLEKGAIVLSLSD 340
DB 242 SEIRPEATGYGAVLFVENVLKDGESLKGKRCIVSGAGNVAQYCAELLLEKGAIVLSLSD 301
```

Db 242 SEIRPEATGYGAVLVFENVVLKDKGESLKGKRLVSGAGNVAQYCAELLLEKGAIVLSLSD 301  
Qy 341 SQGVYVPENGFTTRBOLAQVDMKKNSARISEYKSDPTAVYVGRRKWEIQCVDIAFP 400  
Db 302 SQGVYVPENGFTTRBOLAQVDMKKNSARISEYKSDPTAVYVGRRKWEIQCVDIAFP 361  
Qy 401 CATONEIDEHDAELLIKGCOYVVEGAMNPSTNEAIHKYNKAGIYCPGKAANGVAVS 460  
Db 362 CATONEIDEHDAELLIKGCOYVVEGAMNPSTNEAIHKYNKAGIYCPGKAANGVAVS 421  
Qy 461 GLENTORMSLMTREVRDLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 520  
Db 422 GLENTORMSLMTREVRDLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAV 481  
Qy 521 KAOGAV 526  
Db 482 KAOGAV 487

## RESULT 7

US-08-541-033A-26  
Sequence 26, Application US/08541033A  
Patent No. 5879941  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
NUMBER OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-541-033A-26

Query Match 90.6%; Score 2465; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 2,6e-219;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 51 MDATTGPTALQKVKQMATKAGTEGLVHGKNDVROLTEIMKXDPDOOEFPQAVREV 110  
Db 1 MDATTGPTALQKVKQMATKAGTEGLVHGKNDVROLTEIMKXDPDOOEFPQAVREV 60  
Qy 111 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGRFVQYSSAIGPYK 170  
Db 61 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGRFVQYSSAIGPYK 120

Qy 171 GLRHPESVNLIMKFLAFEOIFKNSLTTLLPMGGKGSDDPKKSDAEVNRFCOSFMT 230  
Db 121 GLRHPESVNLIMKFLAFEOIFKNSLTTLLPMGGKGSDDPKKSDAEVNRFCOSFMT 180  
Qy 231 LQRHISYVQDVVPADIGVGAREIGYLFQYKRTITKNTGVLTJPKQDEYGSSEIRPEATGY 290  
Db 181 LQRHISYVQDVVPADIGVGAREIGYLFQYKRTITKNTGVLTJPKQDEYGSSEIRPEATGY 240  
Qy 291 GAVLFVENVLKDGESEIKGKRLVSGAGNVAQYCAELLLEKGAIVLSLSQGVYVPENG 350  
Db 241 GAVLFVENVLKDGESEIKGKRLVSGAGNVAQYCAELLLEKGAIVLSLSQGVYVPENG 300  
Qy 351 FTREBOLAQVDMKKNSARISEYKSDPTAVYVGRRKWEIQCVDIAFPQATONEIDEH 410  
Db 301 FTREBOLAQVDMKKNSARISEYKSDPTAVYVGRRKWEIQCVDIAFPQATONEIDEH 360  
Qy 411 DAEILLIKGCOYVVEGAMNPSTNEAIHKYNKAGIYCPGKAANGVAVSGLLENTORMS 470  
Db 361 DAEILLIKGCOYVVEGAMNPSTNEAIHKYNKAGIYCPGKAANGVAVSGLLENTORMS 420  
Qy 471 LMTREVRDLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAOGAV 526  
Db 421 LMTREVRDLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAOGAV 476

## RESULT 8

US-08-828-451-26  
Sequence 26, Application US/08828451  
Patent No. 5985634  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
NUMBER OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,451  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,033  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UP155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-828-451-26

Query Match 90.6%; Score 2465; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 2,6e-219;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 MDATTGDFALQKAKWQATKAGTEGLVHG1KNDVRLTLEIFMKDPEQOEFMQAVREV 110  
Db 1 MDATTGDFTLQKAVKQMATKAGTEGLVHG1KNDVRLTLEIFMKDPEQOEFMQAVREV 60  
QY 111 AVSLQPVFEKREPELLP1FKQIVPERVITTRVSVLDDAGN1QVNRGRVVOSSA1GPKG 170  
Db 61 AVSLQPVFEKREPELLP1FKQIVPERVITTRVSVLDDAGN1QVNRGRVVOSSA1GPKG 120  
QY 171 GLRHPVSNVLSIMKFLPEQ1FKNSLTLTPMGGKGSDDPPKKSDAEVRFCQSFMT 230  
Db 121 GLRHPVSNVLSIMKFLPEQ1FKNSLTLTPMGGKGSDDPPKKSDAEVRFCQSFMT 180  
QY 231 LQRRHISYVODVPAGDIGVAREIGYLFQYKRI1KNTGVLT1PKQOEYGSSEIRPEATGY 290  
Db 181 LQRRHISYVODVPAGDIGVAREIGYLFQYKRI1KNTGVLT1PKQOEYGSSEIRPEATGY 240  
QY 291 GAVLFVENVLKDKESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSQGYVPEPNG 350  
Db 241 GAVLFVENVLKDKESLKGKRCCLVSGAGNVAQYCAELLLEKGAIVLSLSQGYVPEPNG 300  
QY 351 FTREQLQAVODMKKQNSARISEYKSDTA1VYVGRKRPWELDCQVDIAFPATONEIDEH 410  
Db 301 FTREQLQAVODMKKQNSARISEYKSDTA1VYVGRKRPWELDCQVDIAFPATONEIDEH 360  
QY 411 DAEILLIKHCQYVVEGANMPESTNEAIHKYNKAGI1YCPKKAANGVAVSGLEMTQNRMS 470  
Db 361 DAEILLIKHCQYVVEGANMPESTNEAIHKYNKAGI1YCPKKAANGVAVSGLEMTQNRMS 420  
QY 471 LNMTRREVRDKLEIMKDIYDSANGPSRRVVDLAAGN1AGFTKVADAVAKQAV 526  
Db 421 LNMTRREVRDKLEIMKDIYDSANGPSRRVVDLAAGN1AGFTKVADAVAKQAV 476

## RESULT 9

US-09-252-991A-20646  
; Sequence 20646, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20646  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20646

Query Match 48.1%; Score 1309; DB 4; Length 450;

Best Local Similarity 59.2%; Pred. No. 2.2e-112;

Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 86 VRQLLLEIFMKDPEQOEFMQAVREVAVSLQVFEKREPELLP-1FKQIVPERVITTRVS 143  
Db 10 VDAFLRLKRRDPQPEFHQAVEVLSLWPFLEANPHYLEAGI1ERIVERALIRFPV 69  
QY 144 WLDAGN1QVNRGRVVOSSA1GPKGGLRHPVSNVLSIMKFLAEQ1FKNSLTLTPMG 203  
Db 70 WVDQGVAVNRGRVVOSSA1GPKGGLRHPVSNVLSIMKFLAEQ1FKNSLTLTPMG 129  
QY 204 GKGSSDDPPKKSDAEVRFCQSFMTLQRRHISYVODVPAGDIGVAREIGYLFQYKRI 263  
Db 130 GKGSSDDPPKKSDAEVRFCQSFMTLQRRHISYVODVPAGDIGVAREIGYLFQYKRI 189  
QY 264 TKNTYGVLT1PKQOEYGSSEIRPEATGYAVLFVENVLKDKESLKGKRCCLVSGAGNVAQY 323

Db 190 SNOFTSVLTGKGSYSGSLR1PEATFGCYFAQEM1KRGRCFPDQORVA1SSSGNVAQY 249  
QY 324 CAELLLEKGAIVLSLSQGYVPEPNGFTREQLQAVODMKKQNSARISEYKSDTA1VYV 363  
Db 250 AARKVMEGKGV1SLDSSEGT1LAENG1SLDEQNEY1MELKNVR-GRIRMAQFSLQFL 308  
QY 384 DRKRPWELDCQVDIAFPATONEIDEHDAELL1KHCQYVVEGANMPESTNEAIHKYNKAG 443  
Db 309 EGRHPVGLAC--DIALPCATQNELDAEDARRLLANGCVCAEGANMPSLTLEAVDLFLEAG 366  
QY 444 IYCPKKAANGVAVSGLEMTQNRMSLWTRREVRDKLEIMKDIYDS-1WPSRRVYV 502  
Db 367 IYCPKKAANGVAVSGLEMTQNRMSLWTRREVRDKLEIMKDIYDS-1WPSRRVYV 426  
QY 503 DLAAGN1AGFTKVADAVAKQAV 526  
Db 427 NYKGANIAGFTKVADAVAKQAV 450

## RESULT 10

US-09-328-352-5725  
; Sequence 5725, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: CTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328.352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5725  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5725

Query Match 46.2%; Score 1257.5; DB 4; Length 467;

Best Local Similarity 55.9%; Pred. No. 1.4e-107;

Matches 255; Conservative 61; Mismatches 128; Indels 13; Gaps 5;

QY 77 LVH-----G1KNDVRLTLEIFMKDPEQOEFMQAVREVAVSLQVFEKREPELLP-1F 128  
Db 11 LHVYAEEDRALKYNINNEFLIN1VQARDPHQPEFLQAVEEWM1SWPFIEKNPEYARQGL 70  
QY 129 KOIVPERVITTRVSVLDDAGN1QVNRGRVVOSSA1GPKGGLRHPVSNVLSIMKFLAE 188  
Db 71 ERIVEPERVITTRVSVLDDAGN1QVNRGRVVOSSA1GPKGGLRHPVSNVLSIMKFLAE 130  
QY 189 EQ1FKNSLTLTPMGGKGSDDPPKKSDAEVRFCQSFMTLQRRHISYVODVPAGDIGV 248  
Db 131 EQ1FKNSLTLTPMGGKGSDDPPKKSDAEVRFCQSFMTLQRRHISYVODVPAGDIGV 190  
QY 249 GAREIGYLFQYKRI1KNTGVLT1PKQOEYGSSEIRPEATGYAVLFVENVLKDKESL 308  
Db 191 GAREIGYLFQYKRI1KNTGVLT1PKQOEYGSSEIRPEATGYAVLFVENVLKDKESL 250  
QY 309 GRCCLVSGAGNVAQYCAELLLEKGAIVLSLSQGYVPEPNGFTREQLQAVODMKKQNS 368  
Db 251 GKTVSISSGAGNVAQYCAELLLEKGAIVLSLSQGYVPEPNGFTREQLQAVODMKKQNS 309  
QY 369 ARISEYKSDTA1VYVGRKRPWELDCQVDIAFPATONEIDEHDAELL1KHCQYVVEGAN 428  
Db 310 GR1SEFASKRGFEYFECKTPMH1--EVDIALPCATQNELTGEAKTLIANGVCAEGAN 367  
QY 429 MPSTNEAIHKYNKAGI1YCPKKAANGVAVSGLEMTQNRMSLWTRREVRDKLEIMKDI 488  
Db 368 MPSTNEAIHKYNKAGI1YCPKKAANGVAVSGLEMTQNRMSLWTRREVRDKLEIMKDI 427  
QY 489 IYDSAM--GPSRRVYVVDLAAGN1AGFTKVADAVAKQAV 524  
Db 428 IHANCVRYGTKEGDTVYVDGANIAGFTKVADAVAKQAV 465



## RESULT 11

US-09-134-000C-3884

Sequence 3884, Application US/09134000C  
Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIORITY APPLICATION NUMBER: US 60/055,778

PRIORITY FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3884

LENGTH: 448

TYPE: PR

ORGANISM: Enterococcus faecalis

US-09-134-000C-3884

Query Match 45.4%; Score 1234.5; DB 4; Length 448;  
Best Local Similarity 55.9%; Pred. No. 1.7e-105;  
Matches 250; Conservative 63; Mismatches 123; Indels 11; Gaps 6;

QY 86 VRLLTEIFMKDPQOEPMQAVREAVASLOPVEKRELLP--IFKQIYPERVITRVS 143

DB 7 VKNIOEKHQDQOCTEYLQAVDEFLPVEGFLFNKPNQYIEANVGLVIEPERIFQFRVP 66

QY 144 WLDAGNLQVNRGRVQVSSAIGPKGGLRPHPSVNLIMKFLAFOIFKNSLTLLPMG 203

DB 67 WODQGMHVRGRVQVNSAIGPKGGLRPHPSVNLIMKFLAFOIFKNSLTLLPMG 126

QY 204 GKGSDPDPKGSAPAEVWRFQSFMTLORHISYVODVPAGDIGVAREIGYLFQYKRI 263

DB 127 GKGSDPDPKGSAPAEVWRFQSFMTLOKHIGSTVDPADIGVAREIGYLFQYKRI 186

QY 264 TKNYTVLTPKQEGYSEIRPEATGYAVLFVENVLKDGESLKGRCCLVSGANVAOY 323

DB 187 RNYDAGVLTGKPLGFGSLRPEATGYAVLYTEEMLKANONSPAGKVVIVSGGNAOY 247

QY 324 CAELLEKGAIVLSLSQGYVIEPNFTREQLQAVODMKKNSAISSEKSTAYVYG 383

DB 247 AMERATLGAIVTIVSDSNQYVIDENGI--DPLDVAIVKERR-ARLEYAKATATY 303

QY 382 VGDRRKPEMLDQVDFAPCATONEIDEHDAELIKHGQVYVVEGANMSTNEAIHKYK 441

DB 303 Y-DKESVWNEFTAYDIALPCATONEINEKQAAIIVKGVKVAAGANMPTLEAVAFK 361

QY 442 AGIYCPKAAAGVAVSGLEMTQNRMSLNTREBVDKLERIMDIYDSAMGSPRRYV 501

DB 362 SAVIYCPKAAAGVAVSALEMSQNSLNTREBVDRLDINININTAKTTSETYGLD 423

QY 502 V--DLAAGNINIGFTKVADVAQAQAV 526

DB 422 ARDNFVIGANVAGFEKVAAMLSHGLV 448

## RESULT 12

US-09-583-110-4489

Sequence 4489, Application US/09583110  
Patent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

FILE REFERENCE: PAT00-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: US 09/107,433

PRIORITY FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 4489

LENGTH: 448

TYPE: PR

ORGANISM: Streptococcus pneumoniae

US-09-583-110-4489

Query Match 44.9%; Score 1221; DB 4; Length 448;  
Best Local Similarity 55.7%; Pred. No. 3.1e-104;  
Matches 248; Conservative 64; Mismatches 125; Indels 8; Gaps 4;

QY 86 VRLLTEIFMKDPQOEPMQAVREAVASLOPVEKRELLP--IFKQIYPERVITRVS 143

DB 8 IQSVFTVKARNGHEAFLOAVEEFMTLPVEKHEDEYIEENTILARITEPERVVSFRVP 67

QY 144 WLDAGNLQVNRGRVQVSSAIGPKGGLRPHPSVNLIMKFLAFOIFKNSLTLLPMG 203

DB 68 WVDKDKIQVNRGRVQVNSAIGPKGGLRPHPSVNLIMKFLAFOIFKNSLTLLPMG 127

QY 204 GKGSDPDPKGSAPAEVWRFQSFMTLORHISYVODVPAGDIGVAREIGYLFQYKRI 263

DB 128 GKGSDPDPKGSAPAEVWRFQSFMTLOKHIGSTVDPADIGVAREIGYLFQYKRI 187

QY 264 TKNYTVLTPKQEGYSEIRPEATGYAVLFVENVLKDGESLKGRCCLVSGANVAOY 323

DB 188 NQFAGVLTGKPLGFGSLRPEATGYAVLYTEEMLKANONSPAGKVVIVSGGNAOY 247

QY 324 CAELLEKGAIVLSLSQGYVIEPNFTREQLQAVODMKKNSAISSEKSTAYVYG 383

DB 248 ALQATLGAIVTIVSDSNQYVIDENGI--DPLDVAIVKERR-ARLEYAKATATY 303

QY 384 DRRKPEMLDQVDFAPCATONEIDEHDAELIKHGQVYVVEGANMSTNEAIHKYK 443

DB 304 HEGTWTYAGNYDIALPCATONEINEKQAAIIVKGVKVAAGANMPTLEAVAFK 363

QY 444 IYCPKAAAGVAVSGLEMTQNRMSLNTREBVDKLERIMDIYDSAMGSPRRYV 502

DB 364 IYCPKAAAGVAVSALEMSQNSLNTREBVDRLDINININTAKTTSETYGLD 423

QY 503 --DLAAGNINIGFTKVADVAQAQAV 526

DB 424 KDVLAGANVAGFEKVAAMLSHGLV 448

## RESULT 13

US-08-886-640-3

Sequence 3, Application US/0886640  
Patent No. 5998700

GENERAL INFORMATION:

APPLICANT: Lightfoot, David

APPLICANT: Long, Lynn

TITLE OF INVENTION: PLANTS CONTAINING THE gdhA GENE AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison &amp; Sutro, L.L.P.

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: United States

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/886,640

FILING DATE: 01-JUL-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/021,058  
FILING DATE: 02-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kokulie, Paul K.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 81163/241766  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)-861-3503  
TELEFAX: (202)-822-0944  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 447 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-886-640-3

Query Match 44.2%; Score 1201; DB 2; Length 447;  
Best Local Similarity 54.0%; Pred. No. 2.2e-102;  
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 86 VRQLTEIFMKDPEQEFMVAAREVAVSLQVEKPEL--LPFKQIYPERVITFRVS 143  
DB 7 LESFLNHVQKRDPNQTEFAQAVREVMVTLMPFLQNPVKRQMSLRLRVEPERVIGRRV 66  
QY 144 WLDAGMLQVNRGRVQYSSAIGPYKGLRPHSVNLSIMKFLAFQIFKNSLITLPMG 203  
DB 67 WVDNRNOIQNRRMRVQFSSAIGPYKGMFRHPSVNLSTIKFLGFQTFKNAITLTPMG 126  
QY 204 GKGSDDPDKSKDAEVRFCQSFMTLORHISVYODVPAGDVGAREIGYLFQYKRI 263  
DB 127 GKGSDDPDKSKSGEYMRFCQALMTLYRHLGADTDVPAGDVGAREIGYLFQYKRI 186  
QY 264 TKNYTGLTPKQGEYSEIRPEATGYAVLFEVENVLKQGESLKGKRCVSGAGNVAQY 323  
DB 187 SNNYACVFTGKLSFGSLIRPEATGYGLVYFTEAMLKRGHMGEGMRVSVSSGNAQY 246  
QY 324 CAELLLEKGAIVLSLDSQGYVTEPNQFTREQLQAVODMKKNSARISYKDTAVYG 383  
DB 247 AIEKMEFGARVITASSSGTVVDESGETKEKLARLIEI-KASRDQVADYAKEFGVYL 305  
QY 384 DRKPEWELDQVDAIPFCATONEIDEHDAELLIKHGQYVVEGAMPSTNEAIIHKYNKAG 443  
DB 306 EGQPMSL--PVDIALPCATONEIDVDAAHQLIANGVAVABGANPFTTEATELFOQAG 363  
QY 444 IIVCPKANAAGVAVSGLEMTQNRMSLNTREBVRDKLERIMKDIYDSAM--GPSRRY 500  
DB 364 VLFAPGANAAGVAVSGLEMAQNAARLGWAKKAVDARLHIMLDIHACVHDGGEQGT 423  
QY 501 NVDLAAGANTAGFTKADAVAKAGAV 526  
DB 424 N--YVQGANIAGFVKVADAMLAQGI 447

RESULT 14  
US-08-884-235-11  
Sequence 11, Application US/08884235  
Patent No. 6329573  
GENERAL INFORMATION:  
APPLICANT: Lightfoot, David A.  
APPLICANT: Long, Lynn M.  
APPLICANT: Lightfoot, Maria E. Vidal  
TITLE OF INVENTION: PLANTS CONTAINING THE gdhA GENE AND  
METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington

STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/884,235  
FILING DATE: 27-JUN-1997  
CLASSIFICATION: 800  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 447 residues  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-884-235-11

Query Match 44.2%; Score 1201; DB 3; Length 447;  
Best Local Similarity 54.0%; Pred. No. 2.2e-102;  
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 86 VRQLTEIFMKDPEQEFMVAAREVAVSLQVEKPEL--LPFKQIYPERVITFRVS 143  
DB 7 LESFLNHVQKRDPNQTEFAQAVREVMVTLMPFLQNPVKRQMSLRLRVEPERVIGRRV 66  
QY 144 WLDAGMLQVNRGRVQYSSAIGPYKGLRPHSVNLSIMKFLAFQIFKNSLITLPMG 203  
DB 67 WVDNRNOIQNRRMRVQFSSAIGPYKGMFRHPSVNLSTIKFLGFQTFKNAITLTPMG 126  
QY 204 GKGSDDPDKSKDAEVRFCQSFMTLORHISVYODVPAGDVGAREIGYLFQYKRI 263  
DB 127 GKGSDDPDKSKSGEYMRFCQALMTLYRHLGADTDVPAGDVGAREIGYLFQYKRI 186  
QY 264 TKNYTGLTPKQGEYSEIRPEATGYAVLFEVENVLKQGESLKGKRCVSGAGNVAQY 323  
DB 187 SNNYACVFTGKLSFGSLIRPEATGYGLVYFTEAMLKRGHMGEGMRVSVSSGNAQY 246  
QY 324 CAELLLEKGAIVLSLDSQGYVTEPNQFTREQLQAVODMKKNSARISYKDTAVYG 383  
DB 247 AIEKMEFGARVITASSSGTVVDESGETKEKLARLIEI-KASRDQVADYAKEFGVYL 305  
QY 384 DRKPEWELDQVDAIPFCATONEIDEHDAELLIKHGQYVVEGAMPSTNEAIIHKYNKAG 443  
DB 306 EGQPMSL--PVDIALPCATONEIDVDAAHQLIANGVAVABGANPFTTEATELFOQAG 363  
QY 444 IIVCPKANAAGVAVSGLEMTQNRMSLNTREBVRDKLERIMKDIYDSAM--GPSRRY 500  
DB 364 VLFAPGANAAGVAVSGLEMAQNAARLGWAKKAVDARLHIMLDIHACVHDGGEQGT 423  
QY 501 NVDLAAGANTAGFTKADAVAKAGAV 526  
DB 424 N--YVQGANIAGFVKVADAMLAQGI 447

RESULT 15  
US-08-370-193A-11  
Sequence 11, Application US/08370193A  
Patent No. 5573945  
GENERAL INFORMATION:  
APPLICANT: ONO, BIJI  
APPLICANT: TSUJIMOTO, NOBUHARU  
APPLICANT: MATSUI, KAZUHIKO  
APPLICANT: KURAHASHI, KAZUHIKO  
TITLE OF INVENTION: MUTANT AND METHOD FOR PRODUCING  
L-GLUTAMIC ACID BY FERMENTATION  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent'n Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,193A  
FILING DATE: 09-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-714-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
TELEX: 248855 OPTAT UR  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 447 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-370-193A-11

Query Match 44.1%; Score 1200; DB 1; Length 447;  
Best Local Similarity 54.0%; Pred. No. 2.7e-102;  
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 86 VRQLLEIFMKDPQOEFMQAVREVAVSLQPFKEPEL--LPFKQIVPEERYITFRVS 143  
DB 7 LESFLNHVQKRDPNTEFAQVREVMWTLWPFLEQNPYRQMSLERLVEREVIQFRVV 66  
QY 144 WLDNAGNLQVNRGRVQYSSAIGPYKGLRPHPSVNLSTMKFLAEQIFKNSLTLLPMG 203  
DB 67 WVDNRNOIQVNRARVQFSSAIGPYKGMRPHSPVNLSTLFLQFEQTFKNALTTLLPMG 126  
QY 204 GKGSDFDPKGSDAEVRFCOSFMTLQRIHSYVQDPAGDIGVAREIGYLFQYKRI 263  
DB 127 GKGSDDFDPKGSSEGEVWRFQALMTLRYHLGADTVDPAGDIGVAREIGVFMAGMKQL 186  
QY 264 TKNYTGVLTPEKQYSGSEIRPEATGYAVLFVENVLKDKGESLKGKCLVSGAGNVAQY 323  
DB 187 SNNTACVFTGKGLSPGSLIRPEATGYLVFTFAMLKRGHMGPEGRVSVSSGNAQY 246  
QY 324 CAELLEKGAIVLSLDSQGYVYEPNCFTRQLOAVODMKKKNSARISEYKSDTAVYVG 383  
DB 247 AIEKAMEFGARVITYASDSGTVDGSGFTKEKLRLIEI-KASRDGRVADYAKEFGLVYL 305  
QY 384 DRKPEWELDCQVDIAPCATONEIDEHDAELLIKGCQYVEGAMPTNEAIHKYNKAG 443  
DB 306 EGQQPMSL--PVDIALPCATNELDVAHQLIANGVAVAEGAMPTTEATELFOQAG 363  
QY 444 ILYPCGAANAGVAVSGLEMTQNRMSLMTREVRDRLERIMKOIYDSAM--GPSRY 500  
DB 364 VLFAPGRDANAGVATSGLEMPQNAARIGWKAKEKVDARLHIMLDIHHACVHEHGSEGT 423  
QY 501 NVDLAAGANTAGFTKVADAVKAGAV 526  
DB 424 N--YVQGANIAGFVKVADAMLAQGI 447

Search completed: July 9, 2005, 18:36:41  
Job time : 45 secs

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OM protein - protein search, using sw model1

Run on: July 9, 2005, 18:29:13 ; Search time 166 Seconds

(without alignments)  
1224.155 Million cell updates/sec

Title: US-10-627-886-2

Perfect score: 2720

Sequence: 1 MGNALVAKPVAAPLAARPR.....GANIAGFTKVADAVKAGAV 526

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubppaa/PCRT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubppaa/PCRTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubppaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubppaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubppaa/US10A\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubppaa/US10E\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubppaa/US10F\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubppaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2720	100.0	526	US-09-070-844-2	Sequence 2, Appl1
2	2720	100.0	526	US-10-627-886-2	Sequence 2, Appl1
3	2621	96.4	512	US-09-070-844-4	Sequence 4, Appl1
4	2621	96.4	512	US-10-627-886-4	Sequence 4, Appl1
5	2508	92.2	487	US-09-070-844-24	Sequence 24, Appl1
6	2508	92.2	487	US-10-627-886-24	Sequence 24, Appl1
7	2465	90.6	476	US-09-070-844-26	Sequence 26, Appl1
8	2465	90.6	476	US-10-627-886-26	Sequence 26, Appl1
9	1309	48.1	445	US-10-282-122A-66687	Sequence 66687, A
10	1297.5	47.7	444	US-10-282-122A-65129	Sequence 65129, A
11	1294.5	47.6	444	US-10-282-122A-66041	Sequence 66041, A

12	1294.5	47.6	444	US-10-275-026A-152	Sequence 152, App
13	1287.5	47.3	449	US-10-282-122A-67538	Sequence 67538, A
14	1281	47.1	445	US-10-369-493-13947	Sequence 13947, A
15	1259	46.3	454	US-10-369-493-9839	Sequence 9839, App
16	1257.5	46.2	462	US-10-282-122A-45200	Sequence 45200, A
17	1239.5	45.6	448	US-10-282-122A-57310	Sequence 57310, A
18	1238	45.5	449	US-10-260-877-90	Sequence 90, Appl1
19	1238	45.5	449	US-10-282-122A-58096	Sequence 58096, A
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21	1230	45.2	449	US-10-282-122A-66870	Sequence 66870, A
22	1214	44.6	448	US-10-282-122A-74024	Sequence 74024, A
23	1212	44.5	448	US-10-472-928-2632	Sequence 2632, App
24	1210.5	44.5	458	US-10-369-493-17284	Sequence 17284, A
25	1207.5	44.4	464	US-10-282-122A-51278	Sequence 51278, A
26	1205.5	44.3	444	US-10-369-493-617	Sequence 617, App
27	1205.5	44.3	444	US-10-282-122A-48442	Sequence 48442, A
28	1201	44.2	447	US-10-369-493-859	Sequence 859, App
29	1199	44.2	447	US-10-282-122A-43284	Sequence 43284, A
30	1199	44.1	443	US-10-282-122A-52117	Sequence 52117, A
31	1196.5	44.0	466	US-10-425-114-72961	Sequence 72961, A
32	1195.5	44.0	468	US-10-369-493-8215	Sequence 8215, App
33	1194	43.9	438	US-10-369-493-10621	Sequence 10621, A
34	1194	43.8	447	US-10-369-493-10621	Sequence 60243, A
35	1185	43.6	447	US-09-738-626-6982	Sequence 6982, App
36	1182.5	43.5	448	US-10-282-122A-53998	Sequence 53998, A
37	1181	43.4	447	US-10-282-122A-75593	Sequence 75593, A
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39	1180	43.4	447	US-10-369-493-295	Sequence 295, App
40	1178	43.3	447	US-10-282-122A-72769	Sequence 72769, A
41	1177.5	43.3	446	US-10-282-122A-68627	Sequence 68627, A
42	1169.5	43.0	446	US-10-282-122A-62874	Sequence 62874, A
43	1169	43.0	442	US-10-282-122A-55644	Sequence 55644, A
44	1153	42.4	447	US-10-282-122A-78288	Sequence 78288, A
45	1150	42.3	448	US-10-282-122A-58700	Sequence 58700, A

#### ALIGNMENTS

RESULT 1  
US-09-070-844-2  
Sequence 2, Application US/09070844  
Patent No. US20020062495A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanichik & Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/09/070,844  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,596  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (904) 375-8100  
 TELEFAX: (904) 372-5800  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 526 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-070-844-2

Query Match 100.0%; Score 2720; DB 9; Length 526;  
 Best Local Similarity 100.0%; Pred. No. 5,7e-236;  
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MOTLVAKPIVAAPLAARPCLAAPWPCAMWSAKRDVRAKVSLEBQISAMDATTGDTFTA 60
DB 1 MOTLVAKPIVAAPLAARPCLAAPWPCAMWSAKRDVRAKVSLEBQISAMDATTGDTFTA 60
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DB 61 LQKAVKQMATKATGTEGLVHGINKPDVROLTEIFMKDPEQOEPMQAVREVAVSLQPVFEK 120
QY 121 RPBLPIFKQIVPERVITFRVSWLDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 180
DB 121 RPBLPIFKQIVPERVITFRVSWLDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 180
QY 181 SIMFLAFEOIFKNSLTLLPMGGKGSDFDPKGSDAEVMRFQOSFTELQRIHSIVYOD 240
DB 181 SIMFLAFEOIFKNSLTLLPMGGKGSDFDPKGSDAEVMRFQOSFTELQRIHSIVYOD 240
QY 241 VPAGDIGVAREIGYLFQGYKRIITKNYTGVLTPKGOEYGSSEIRPEATGYAVLFVENVL 300
DB 241 VPAGDIGVAREIGYLFQGYKRIITKNYTGVLTPKGOEYGSSEIRPEATGYAVLFVENVL 300
QY 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGFTRBOLQAVQ 360
DB 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGFTRBOLQAVQ 360
QY 361 DMKKKNSARISEYKSDTAAYVVDGRKRWELDCQVDIAFPICATONEIDEHDAELLIKHGC 420
DB 361 DMKKKNSARISEYKSDTAAYVVDGRKRWELDCQVDIAFPICATONEIDEHDAELLIKHGC 420
QY 421 QYVEGANMPSTNEAIHKYNKAGIICPGKAAAGVAVSGLEMTQNRMSLMTREVRD 480
DB 421 QYVEGANMPSTNEAIHKYNKAGIICPGKAAAGVAVSGLEMTQNRMSLMTREVRD 480
QY 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGAV 526
DB 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGAV 526

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## RESULT 2

US-10-627-886-2  
 Sequence 2, Application US/10627886  
 Publication No. US20040128710A1

GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

INVENTOR: Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
 RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE  
 DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/627,886  
 FILING DATE: 24-Jul-2003  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/070,844  
 FILING DATE: 01-MAY-98  
 APPLICATION NUMBER: 08/725,596  
 FILING DATE: 03-OCT-96  
 APPLICATION NUMBER: 08/541,033  
 FILING DATE: 06-OCT-95  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lloyd, Jeff  
 REGISTRATION NUMBER: 35,589  
 REFERENCE/DOCKET NUMBER: UF-155CD3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (352) 375-8100  
 TELEFAX: (352) 372-5800  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 526 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-627-886-2

Query Match 100.0%; Score 2720; DB 16; Length 526;  
 Best Local Similarity 100.0%; Pred. No. 5,7e-236;  
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MOTLVAKPIVAAPLAARPCLAAPWPCAMWSAKRDVRAKVSLEBQISAMDATTGDTFTA 60
DB 1 MOTLVAKPIVAAPLAARPCLAAPWPCAMWSAKRDVRAKVSLEBQISAMDATTGDTFTA 60
QY 61 LQKAVKQMATKATGTEGLVHGINKPDVROLTEIFMKDPEQOEPMQAVREVAVSLQPVFEK 120
DB 61 LQKAVKQMATKATGTEGLVHGINKPDVROLTEIFMKDPEQOEPMQAVREVAVSLQPVFEK 120
QY 121 RPBLPIFKQIVPERVITFRVSWLDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 180
DB 121 RPBLPIFKQIVPERVITFRVSWLDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 180
QY 181 SIMFLAFEOIFKNSLTLLPMGGKGSDFDPKGSDAEVMRFQOSFTELQRIHSIVYOD 240
DB 181 SIMFLAFEOIFKNSLTLLPMGGKGSDFDPKGSDAEVMRFQOSFTELQRIHSIVYOD 240
QY 241 VPAGDIGVAREIGYLFQGYKRIITKNYTGVLTPKGOEYGSSEIRPEATGYAVLFVENVL 300
DB 241 VPAGDIGVAREIGYLFQGYKRIITKNYTGVLTPKGOEYGSSEIRPEATGYAVLFVENVL 300
QY 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGFTRBOLQAVQ 360
DB 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGFTRBOLQAVQ 360
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DB 361 DMKKKNSARISEYKSDTAAYVVDGRKRWELDCQVDIAFPICATONEIDEHDAELLIKHGC 420
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QY 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGAV 526
DB 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGAV 526

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## RESULT 3

US-09-070-844-4  
 Sequence 4, Application US/09070844



Patent No. US20020062495A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,844  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,596  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-844-4  
Query Match 96.4%; Score 2621; DB 9; Length 512;  
Best Local Similarity 97.3%; Pred. No. 4.6e-227;  
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
QY 1 MOTALVAKPIVAAPLAPRCLAPWPCAWRSARADVAKAVSLSEBOISAMDATGDPFTA 60  
DB 1 MOTALVAKPIVA-----CAWRSARADVAKAVSLSEBOISAMDATGDPFTA 46  
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DB 47 LQKAVKQMATKATGEGVLHGINKPDVROLTEIFMKDPEQEFMQAVREVAVSLQPVFEK 106  
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DB 107 RPELLPIFKQIVPERVITFRVSWLDDAGNLQVNRGRVYSSAIGYKGLAFHPSVNL 166  
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DB 167 SIMKFLAFEOIFKNSLTLTPMGSGKSGSDPDKGSDAEVRFCOSFMTTELQRIHSYQD 226  
QY 241 VPADIGVAREIGYLFQGYRITKNTYGVLTTPKQEGYSGSEIRPEATGYAVLFEVNL 300  
DB 227 VPADIGVAREIGYLFQGYRITKNTYGVLTTPKQEGYSGSEIRPEATGYAVLFEVNL 286  
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DB 407 QYVVGAMBPSTNEAIHKYKAGIYYCPGKAANGVAVSGLEMTONRMSLMTREEVRD 466  
QY 481 KLERIMDIYDSAMPSPRRYVNDLAAGANIAGFTKVADAVYAGQAV 526  
DB 467 KLERIMDIYDSAMPSPRRYVNDLAAGANIAGFTKVADAVYAGQAV 512  
RESULT 4  
US-10-627-886-4  
Sequence 4, Application US/10627886  
Publication No. US20040128710A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE  
DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/627,886  
FILING DATE: 24-Jul-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/070,844  
FILING DATE: 01-MAY-98  
APPLICATION NUMBER: 08/725,596  
FILING DATE: 03-OCT-96  
APPLICATION NUMBER: 08/541,033  
FILING DATE: 06-OCT-95  
ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: UF-155CD3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-627-886-4  
Query Match 96.4%; Score 2621; DB 16; Length 512;  
Best Local Similarity 97.3%; Pred. No. 4.6e-227;  
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
QY 1 MOTALVAKPIVAAPLAPRCLAPWPCAWRSARADVAKAVSLSEBOISAMDATGDPFTA 60  
DB 1 MOTALVAKPIVA-----CAWRSARADVAKAVSLSEBOISAMDATGDPFTA 46  
QY 61 LQKAVKQMATKATGEGVLHGINKPDVROLTEIFMKDPEQEFMQAVREVAVSLQPVFEK 120  
DB 47 LQKAVKQMATKATGEGVLHGINKPDVROLTEIFMKDPEQEFMQAVREVAVSLQPVFEK 106  
QY 121 RPELLPIFKQIVPERVITFRVSWLDDAGNLQVNRGRVYSSAIGYKGLAFHPSVNL 180

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Db 107 RPELLPFIKQIVBERVITFRVSWLDDAGNLOVNRGEFVQYSSAIGPYKGLRHPSPVNL 166
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Db 167 SIMKFLAEFOI FKNSLTTLPWGSGKGSDDPKGSDAEVNRFCOSFMTTELORHISYVOD 226
Qy 241 VPADIGVAGABIGLFGQYKRTTKNYTGVLTLPKGOEYSGSEIRPEATGYAVLFVENVL 300
Db 227 VPADIGVAGABIGLFGQYKRTTKNYTGVLTLPKGOEYSGSEIRPEATGYAVLFVENVL 286
Qy 301 KDKESLKGKCLVSGAGNVAQYCAELLEKGALVLSLSDSQGYVEBNGFTREQLQAVQ 360
Db 287 KDKESLKGKCLVSGAGNVAQYCAELLEKGALVLSLSDSQGYVEBNGFTREQLQAVQ 346
Qy 361 DMKKKNSARISEKSDTAVVVGDRRKPWELDCQVDTAFPCATONEIDEHDAELLIRHGC 420
Db 347 DMKKKNSARISEKSDTAVVVGDRRKPWELDCQVDTAFPCATONEIDEHDAELLIRHGC 406
Qy 421 QYVEGANMPTNEAIHKYNKAGIIPCCKAANAGVAVSGLENTONRMSLNTREEVYD 480
Db 407 QYVEGANMPTNEAIHKYNKAGIIPCCKAANAGVAVSGLENTONRMSLNTREEVYD 466
Qy 481 KLERIMKDIYDSAMGSPSRVNVDLAAGANIAGFTKVADAVAKAGAV 526
Db 467 KLERIMKDIYDSAMGSPSRVNVDLAAGANIAGFTKVADAVAKAGAV 512

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## RESULT 5

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US-09-070-844-24
: Sequence 24, Application US/09070844
: Patent No. US20020062495A1
: GENERAL INFORMATION:

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: APPLICANT: Schmidt, Robert R.
: TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
: TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA
: ZIP: 32606

```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/070,844
: FILING DATE:
: CLASSIFICATION:

```

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/725,596
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:

```

```

: NAME: Whitlock, Ted W.
: REGISTRATION NUMBER: 36,965
: REFERENCE/DOCKET NUMBER: UF155
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (904) 375-8100
: TELEFAX: (904) 372-5800

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: INFORMATION FOR SEQ ID NO: 24:

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 487 amino acids
: TYPE: amino acid

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: TOPOLOGY: linear
: MOLECULE TYPE: protein

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: US-09-070-844-24

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Query Match 92.2%; Score 2508; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 6,6e-217;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AVSLSEQISAMDATTGDTFLQKAVKQMATKAGTEGVHGIKNPDVROLTLTIFMDPEQ 61
Qy 101 QEFMQAVREAVASLOPFEERPELPIFKQIVBERVITFRVSWLDDAGNLOVNRGEFVQ 160
Db 62 QEFMQAVREAVASLOPFEERPELPIFKQIVBERVITFRVSWLDDAGNLOVNRGEFVQ 121
Qy 161 YSSAIGPYKGLRHPSPVNLISIMKFLAEFOI FKNSLTTLPWGSGKGSDDPKGSDAEV 220
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Qy 281 SEIRPEATGYAVLFVENVLKDKESLKGKCLVSGAGNVAQYCAELLEKGALVLSLSD 340
Db 242 SEIRPEATGYAVLFVENVLKDKESLKGKCLVSGAGNVAQYCAELLEKGALVLSLSD 301
Qy 341 SOGYVEBNGFTREQLQAVQDMKKKNSARISEKSDTAVVVGDRRKPWELDCQVDTAF 400
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Qy 401 CATONEIDEHDAELLIRHGCQYVEGANMPTNEAIHKYNKAGIIPCCKAANAGVAVS 460
Db 362 CATONEIDEHDAELLIRHGCQYVEGANMPTNEAIHKYNKAGIIPCCKAANAGVAVS 421
Qy 461 GLENTONRMSLNTREEVYDKLERIMKDIYDSAMGSPSRVNVDLAAGANIAGFTKVADAV 520
Db 422 GLENTONRMSLNTREEVYDKLERIMKDIYDSAMGSPSRVNVDLAAGANIAGFTKVADAV 481
Qy 521 KAQAGAV 526
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## RESULT 6

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US-10-627-886-24
: Sequence 24, Application US/10627886
: Publication No. US20040128710A1
: GENERAL INFORMATION:

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: APPLICANT: Schmidt, Robert R.
: TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

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: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
: DEHYDROGENASES AND METHODS OF USE
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:

```

```

: ADDRESSEE: Saliwanchik & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA

```

```

: ZIP: 32606-6669
: COMPUTER READABLE FORM:

```

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: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/627,886

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: FILING DATE: 24-Jul-2003
: CLASSIFICATION: <Unknown>

```

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/070,844

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: FILING DATE: 01-MAY-98
: APPLICATION NUMBER: 08/725,596

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: FILING DATE: 03-OCT-96

```

APPLICATION NUMBER: 08/541,033  
FILING DATE: 06-OCT-95  
ATTORNEY/AGENT INFORMATION:  
NAME: LLOYD, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: UF-155CD3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-10-627-886-24

Query Match 92.2%; Score 2508; DB 16; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6,6e-217;  
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AVSLSEQISAMDATGDFALQKAVKQMATAGTEGLVHGINKPDVROLTEIFMKDPEQ 100  
DB 2 AVSLSEQISAMDATGDFALQKAVKQMATAGTEGLVHGINKPDVROLTEIFMKDPEQ 61  
QY 101 QEFMOAVREVAVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNIQVNRGRVQ 160  
DB 62 QEFMOAVREVAVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNIQVNRGRVQ 121  
QY 161 YSSAIGPYKGLRPHSPVNSIMKFLAPEQIFKNSLTLPMGGKGGSDPFGKSDAEV 220  
DB 122 YSSAIGPYKGLRPHSPVNSIMKFLAPEQIFKNSLTLPMGGKGGSDPFGKSDAEV 181  
QY 221 MRFCQSFMTLQRIHSYQDVPAIDIGVAREIGYLFQYKRITKNTGVLTPKQGEYGG 280  
DB 182 MRFCQSFMTLQRIHSYQDVPAIDIGVAREIGYLFQYKRITKNTGVLTPKQGEYGG 241  
QY 281 SEIRPATGAVAFVENVLKDGESLKGRCLVSGAGNVAQCAELLEKGAIVLSLSD 340  
DB 242 SEIRPATGAVAFVENVLKDGESLKGRCLVSGAGNVAQCAELLEKGAIVLSLSD 301  
QY 341 SQGYVEPNPGRFQOLQAVQDMKKNSARISEYKSDTAVYVGRPKPWEIDCOVDIAFP 400  
DB 302 SQGYVEPNPGRFQOLQAVQDMKKNSARISEYKSDTAVYVGRPKPWEIDCOVDIAFP 361  
QY 401 CATONEIDEHDAELLIRGCOYVEGANMPSSTNEAIHKYNKAGIYCPGKAANAGVAVS 460  
DB 362 CATONEIDEHDAELLIRGCOYVEGANMPSSTNEAIHKYNKAGIYCPGKAANAGVAVS 421  
QY 461 GLENTORMSLNTWREVRDLEIRIMDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAV 520  
DB 422 GLENTORMSLNTWREVRDLEIRIMDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAV 481  
QY 521 KAQAV 526  
DB 482 KAQAV 487

RESULT 7  
US-09-070-844-26  
Sequence 26, Application US/09070844  
Patent No. US20020062495A1  
GENERAL INFORMATION:  
APPLICANT: Schmidt, Robert R.  
APPLICANT: Miller, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Saliwanichik & Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,844  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,596  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Whitlock, Ted W.  
REGISTRATION NUMBER: 36,965  
REFERENCE/DOCKET NUMBER: UF155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-844-26

Query Match 90.6%; Score 2465; DB 9; Length 476;  
Best Local Similarity 100.0%; Pred. No. 4,8e-213;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 MDATGDFALQKAVKQMATAGTEGLVHGINKPDVROLTEIFMKDPEQEFMOAVREV 110  
DB 1 MDATGDFALQKAVKQMATAGTEGLVHGINKPDVROLTEIFMKDPEQEFMOAVREV 60  
QY 111 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNIQVNRGRVQYSSAIGPYK 170  
DB 61 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNIQVNRGRVQYSSAIGPYK 120  
QY 171 GLRPHSPVNSIMKFLAPEQIFKNSLTLPMGGKGGSDPFGKSDAEVMRFCQSFMT 230  
DB 121 GLRPHSPVNSIMKFLAPEQIFKNSLTLPMGGKGGSDPFGKSDAEVMRFCQSFMT 180  
QY 231 LQRIHSYQDVPAIDIGVAREIGYLFQYKRITKNTGVLTPKQGEYGGSEIRPEATGY 290  
DB 181 LQRIHSYQDVPAIDIGVAREIGYLFQYKRITKNTGVLTPKQGEYGGSEIRPEATGY 240  
QY 291 GAVLFEVENVLKDGESLKGRCLVSGAGNVAQCAELLEKGAIVLSLSDSQGYVEPN 350  
DB 241 GAVLFEVENVLKDGESLKGRCLVSGAGNVAQCAELLEKGAIVLSLSDSQGYVEPN 300  
QY 351 FTRFQOLQAVQDMKKNSARISEYKSDTAVYVGRPKPWEIDCOVDIAFCATONEIDEH 410  
DB 301 FTRFQOLQAVQDMKKNSARISEYKSDTAVYVGRPKPWEIDCOVDIAFCATONEIDEH 360  
QY 411 DAEILLIRGCOYVEGANMPSSTNEAIHKYNKAGIYCPGKAANAGVAVSGLLENTORMS 470  
DB 361 DAEILLIRGCOYVEGANMPSSTNEAIHKYNKAGIYCPGKAANAGVAVSGLLENTORMS 420  
QY 471 LNTWREVRDLEIRIMDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQAV 526  
DB 421 LNTWREVRDLEIRIMDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQAV 476

RESULT 8  
US-10-627-886-26  
Sequence 26, Application US/10627886  
Publication No. US20040128710A1  
GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.  
MILLER, Philip  
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES  
RELATING TO THE - AND -SUBUNITS OF GLUTAMATE  
DEHYDROGENASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/627,886  
FILING DATE: 24-Jul-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/070,844  
FILING DATE: 01-MAY-98  
APPLICATION NUMBER: 08/725,596  
FILING DATE: 03-OCT-96  
APPLICATION NUMBER: 08/541,033  
FILING DATE: 06-OCT-95  
ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: UF-155CD3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 372-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-10-627-886-26  
Query Match 90.6%; Score 2465; DB 16; Length 476;  
Best Local Similarity 100.0%; Pred. No. 4.8e-213;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 51 MDATTGDTALQKAKMATKAGTEGLVHGIXNPDVRLQLTEIFMKDPEQOEPMQAVREV 110  
DB 1 MDATTGDTALQKAKMATKAGTEGLVHGIXNPDVRLQLTEIFMKDPEQOEPMQAVREV 60  
QY 111 AVSLQIPVEKRPBELLPIFKQIVPEERYITFRVSWLDAGNIQVNRGRVYSSAIGYK 170  
DB 61 AVSLQIPVEKRPBELLPIFKQIVPEERYITFRVSWLDAGNIQVNRGRVYSSAIGYK 120  
QY 171 GLRHPSPVNSIMKFLAFEOIFKSLTTLPMGGGSGSDPDKKSDAIVRRFCQSPMTE 230  
DB 121 GLRHPSPVNSIMKFLAFEOIFKSLTTLPMGGGSGSDPDKKSDAIVRRFCQSPMTE 180  
QY 231 LQRIHSIVVDVPADIGVAREIGYLFQGYKRIKNTYGVLTLPKQOEYSGSEIRPEATGY 290  
DB 181 LQRIHSIVVDVPADIGVAREIGYLFQGYKRIKNTYGVLTLPKQOEYSGSEIRPEATGY 240  
QY 291 GAVLFEVENVLKDKESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSQGYVYEPNG 350  
DB 241 GAVLFEVENVLKDKESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSQGYVYEPNG 300  
QY 351 FTRQQLAVQDMKKKNSARISEYKSDTAVVGDPRKPMELDQVDAFPQATONEIDEH 410  
DB 301 FTRQQLAVQDMKKKNSARISEYKSDTAVVGDPRKPMELDQVDAFPQATONEIDEH 360

QY 411 DAELLIKHGCQYVEGANMSTNEAIHKYKAGIIPCGRANAGVAVSGLMONTNRMS 470  
DB 361 DAELLIKHGCQYVEGANMSTNEAIHKYKAGIIPCGRANAGVAVSGLMONTNRMS 420  
QY 471 LMTREVRDKLRIMKDIYDSAMGSRRTNVULAAGANTAGETKADAKAGAV 526  
DB 421 LMTREVRDKLRIMKDIYDSAMGSRRTNVULAAGANTAGETKADAKAGAV 476  
RESULT 9  
US-10-282-122A-66687  
Sequence 66687, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 66687  
LENGTH: 445  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-10-282-122A-66687  
Query Match 48.1%; Score 1309; DB 15; Length 445;  
Best Local Similarity 59.2%; Pred. No. 7.3e-109;  
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;  
QY 86 VRQLLEIFMKDPEQOEPMQAVREAVSLQPVKRPBELLPIFKQIVPEERYITFRV 143  
DB 5 VDAFLERLKRDDQDFPHQAVEVLRSLMPLFANPHYLEAGIIEIVPEERAILFRVP 64  
QY 144 WLDDAGNLQVNRGFRVYSSAIGPYKGLRFPBVSNIIMKFLAFEOIFKSLTTLPMGG 203  
DB 65 WVDQGRVRRNRRYVRQMSAIGPYKGLRFPBVSNIIMKFLAFEOIFKSLTTLPMGG 124  
QY 204 GKGGSDPDKKSDAIVRRFCQSPMTELORIHSIVVDVPADIGVAREIGYLFQGYKRI 263

```

Db      125 GKGSGSDPDKGKSDAEVWRFQCSFMSELVYRHVADLDPVPAIGDVGAREIGYLFQYRL 184
Qy      264 TKNYTVLTTPKQDQYGGSEIRPEATGYGAVLFVENVLKDKGESLKGRCCLVSGAGNVAQ 323
Db      185 SNOGTSVLTGSGYSGSLIRPEATGFCVFADEMUKDRGRGDFGRVALISGSGNVAQ 244
Qy      324 CAELLLEKGAIVLSLSDSGYVEPNFTREQLQAVODMKKNSARISEYKSDTAAYVG 383
Db      245 AARVWMEGKGVILSDSEGLVLAAGLSDQWEMYLKLVNR-GRIRMAEQPSIQFL 303
Qy      384 DRRKPELDCQVDIAFPQATONEIDEHDAELLIKHGCQYVEGANMPSITNEAIHKYNK 443
Db      304 EGRFPWGLAC--DIALPCATQNEIDAEADARLLANGCVCAEGANMPSITLEAVDLPLEAG 361
Qy      444 IIVYCPKAAAGVAVSGLENTQRMSLNWTREVRDKLERIMDIYDSA-MGFSRRYV 502
Db      362 ILVAPGASNAAGVAVSGLEMSQNAMRLRWSEGEVDTLHGIMQSIHHAICLLYSEEGRV 421
Qy      503 DLAAGANIAGFTKVAADVAKQAV 526
Db      422 NYVGANITAGFVKVADMLAQGV 445

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## RESULT 10

US-10-282-122A-65129

Sequence 65129, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

```

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

```

```

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A

```

```

CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remainder Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65129
LENGTH: 444
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65129

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Query Match      47.7%; Score 1297.5; DB 15; Length 444;
Best Local Similarity 57.4%; Pred. No. 7.9e-108;
Matches 257; Conservative 70; Mismatches 106; Indels 15; Gaps 6;

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Qy      85 DVNQLTEIFMKDPEQGEFMAVREAVASIQPYFEKPELL--PIFKQIYEPERVITFRV 142
Db      3 DLNLTFLANLQKRNPNQPFPHQAVEVWMSLDPFLAKNPKYTOQSILERIIVEPERVWFRV 62
Qy      143 SMVDDAGNLQVNGFRQYSSAIGPYKGRPHPSVYVLSIMKFLAFQIRKSLTTLPMG 202
Db      63 TWDDKQGVQVNGYRQVMSAIGPYKGRPHFTYDLGLKFLAFQVFNKALTTLPMG 122
Qy      203 GKGSGSDPDKGKSDAEVWRFQCSFMTELQRIHSYVDVPAIGDVGAREIGYLFQYKR 262
Db      123 GKGSGSDPDKGKSDAEVWRFQCSFMTELQRIHSYVDVPAIGDVGAREIGYLFQYKR 182
Qy      263 ITRNVTGLTPKQDQYGGSEIRPEATGYGAVLFVENVLKDKGESLKGRCCLVSGAGNVAQ 322
Db      183 IRNEFTSVLTGKGLWEGSLIRPEATGCVFPAQMLQTRNDSFEKRVILISGSGNVAQ 242
Qy      323 YCAELLLEKGAIVLSLSDSGYVEPNFTREQLQAVODMKKNSARISEYKSDTAAYV 381
Db      243 YAAEKALQIGAKVILVSDSDGFVLPDIGNTEQLAALIELKEVRRE-RVATYAKEQGLQ 301
Qy      382 VGBRRKPELDCQVDIAFPQATONEIDEHDAELLIKHGCQYVEGANMPSITNEAIHKYNK 441
Db      302 YFENQKPMGV--AAEILPCATQNEIDAEADARLLANGCVCAEGANMPSITLEAVEQPIK 359
Qy      442 AGIIVCPKAAAGVAVSGLENTQRMSLNWTREVRDKLERIMDIYDSAMGPSRRY- 500
Db      360 AGILVAPGASNAAGVAVSGLEMSQNAMRLRWSEGEVDTLHGIMQSIHHSCL---KYG 415
Qy      501 ----NDLAAGANIAGFTKVAADVAKQAV 524
Db      416 KVGDKXVYVVGANITAGFVKVADMLAQG 443

```

## RESULT 11

US-10-282-122A-66041

Sequence 66041, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

```

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

```

```

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A

```

```

CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931

```





```

;
; LENGTH: 445
; TYPE: prt
; ORGANISM: Pseudomonas fluorescens

```

**OY**

144   :         :	WLDAGNLOVNRGFRVOYSATGPYKGLRFPHPSVNLISIMKFLAFEOI FKNLSITLLPMWG	203   :
-------------------------	---	------------

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Db      74  WVDQGVNVRGRVENSAGIPYKGLRHPSPVYLGIIFKLGFBQIFKNSLTGLPIGG 133
Qy      204 GKGSSDFDPKGGDAFVWRFCQSPMTLORHISVYODVPAGDIGVAREIGYLFQYKRI 263
Db      134 GKGSSDFDPKGGSEGEIWRFCQSPITELRYLGDITDVPAGDIGVAREIGYLFQYKRI 193
Qy      264 TKNTYGLTPKQGEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQY 323
Db      194 TNRVEGYLTGKGLTFGGSIGRTATGYGLVFMELKAVGKSPSGATVVSQGNVAIY 253
Qy      324 CAELLLEKGAIVLSLDSQGYVEPNNGFTREQLQAVODMKKNSARISEYKS--DTAVY 381
Db      254 ATQKATQLGGVVAMSDSNGIYDKDGINLDTVRQLKEVERK---RLKDYVSIHPTAEY 309
Qy      382 VGDRKXPMELDCCQVDIAFPACATONEIDEHDAELLKHGCGQYVVEGAMPSTNEAIHKYNK 441
Db      310 YEGCAGIWTIPCA--IAPCATONEIDGAEVAVKNGCTAVGEGANPSTPEAVDVFLQ 367
Qy      442 AGIITYPGKAMAGVAVSGLMTOQRMSLMTREEVYDKLERIMKDIYDSAMGPSRRYN 501
Db      368 HKIITYPGKAMAGVAVSALEMSQNSRVSWTFEEVDATKLKINIMVNIYHNASKAQDFG 427
Qy      502 VD--LAAGANITAGFTYVADAVKAOAV 526
Db      428 FEGNLVAGANITAGFLKVABAMKAOQTV 454

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Search completed: July 9, 2005, 18:39:34  
 Job time : 168 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: July 9, 2005, 18:25:38 ; Search time 42 Seconds  
(without alignments)  
1205.000 Million cell updates/sec

Title: US-10-627-886-2

Perfect score: 2720

Sequence: 1 MOTALVAKPIVAAPLAPR.....GANIAGFTKVADAVKAGAV 526

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2488.5	91.5	523	1	S17949 glutamate dehydrog
2	1324.5	48.7	449	1	A42489 glutamate dehydrog
3	1309	48.1	445	2	H83072 glutamate dehydrog
4	1300.5	47.8	444	2	H81050 glutamate dehydrog
5	1294.5	47.6	444	2	B81825 glutamate dehydrog
6	1238	45.5	449	2	A64053 glutamate dehydrog
7	1214.5	44.7	444	2	T10487 glutamate dehydrog
8	1214	44.6	448	2	D98019 glutamate dehydrog
9	1212	44.5	448	2	H95151 NADP-specific glut
10	1210.5	44.5	458	2	B83912 NADP-specific glut
11	1205.5	44.3	424	2	E75362 glutamate dehydrog
12	1201	44.2	447	1	D85321 glutamate dehydrog
13	1199	44.1	443	2	F66990 NADP-specific glut
14	1198	44.0	447	2	C90937 NADP-specific glut
15	1198	44.0	447	2	G85785 NADP-specific glut
16	1189.5	43.7	458	2	A11503 NADP-specific glut
17	1185	43.6	447	2	S32237 glutamate dehydrog
18	1182	43.5	447	1	A33504 glutamate dehydrog
19	1181	43.4	447	2	AF0710 NADP-specific glut
20	1180.5	43.4	458	2	A11144 NADP-specific glut
21	1153	42.4	447	2	A60483 glutamate dehydrog
22	1150	42.3	448	2	D64567 glutamate dehydrog
23	1143	42.0	450	2	S22403 glutamate dehydrog
24	1142.5	42.0	448	2	B95277 probable glutamate
25	1139	41.9	448	2	F71862 glutamate dehydrog
26	1133.5	41.7	446	1	S06938 glutamate dehydrog
27	1121.5	41.2	454	1	D69388 glutamate dehydrog
28	1115.5	41.0	459	1	S04904 glutamate dehydrog
29	1109	40.8	457	2	S63608 glutamate dehydrog

30	1092	40.1	451	2	T41492 probable glutamate
31	1067.5	39.2	459	2	S17907 glutamate dehydrog
32	1037.5	38.1	454	1	A25275 glutamate dehydrog
33	1022	37.6	457	2	S51960 glutamate dehydrog
34	997.5	36.7	624	2	B96556 hypothetical prote
35	579.5	21.3	416	2	T45284 glutamate dehydrog
36	576.5	21.2	416	2	G72305 glutamate dehydrog
37	557	20.5	424	2	A70055 glutamate dehydrog
38	552.5	20.3	421	2	F83852 glutamate dehydrog
39	545.5	20.1	426	2	G69933 glutamate dehydrog
40	544.5	20.0	414	2	G89862 NAD-specific gluta
41	536	19.7	372	2	G84220 glutamate dehydrog
42	530	19.5	420	2	D75176 glutamate dehydrog
43	529.5	19.5	420	2	F83989 glutamate dehydrog
44	527.5	19.4	430	2	F84142 glutamate dehydrog
45	527.5	19.4	421	2	B81079 glutamate dehydrog

## ALIGNMENTS

## RESULT 1

S17949 glutamate dehydrogenase (NADP) (EC 1.4.1.4) precursor - Chlorella sorokiniana (fragment)

N/Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase

```
Qy 257 FGQYKRTTKYTGVLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSG 316
Dy 254 FGQYKRTTKYTGVLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSG 313
Qy 317 AGNVAQYCAELLLEKGAIVLSLSDSGYVVEPNPFTREQLQAVDMKKKNSARISEYKS 376
Dy 314 AGNVAQYCAELLLEKGAIVLSLSDSGYVVEPNPFTREQLQAVDMKKKNSARISEYKS 373
Qy 377 DTAYVVDNRKRWELDCQVDIAFPKATONEIDEHDAELLKHGGOYVVEGANNPSTNEAI 436
Dy 374 DTAYVVDNRKRWELDCQVDIAFPKATONEIDEHDAELLKHGGOYVVEGANNPSTNEAI 433
Qy 437 HKYKAGIITPCGKAANAGVAVSGLEMTQNRMSLMTREBVDKLRIMKDIYDSAMGP 496
Dy 434 HKYKAGIITPCGKAANAGVAVSGLEMTQNRMSLMTREBVDKLRIMKDIYDSAMGP 493
Qy 497 SRRYVNDLAAGANIAGFTKVAADAVKAQAV 526
Dy 494 SREYVNDLAAGANIAGFTKVAADAVKAQAV 523
```

## RESULT 2

```
A42489
glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Giardia lamblia
N:Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C:Species: Giardia lamblia
C>Date: 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A42489
R:Yee, J.; Dennis, P.P.
J. Biol. Chem. 267, 7539-7544, 1992
A:Title: Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene
A:Reference number: A42489; MUID:92218410; PMID:1559991
A:Accession: A42489
A:Molecule type: DNA
A:Residues: 1-449 <YEE>
A:Cross-references: UNIPROT:P28724; GB:M64604; NID:G159108; PIDN:AAA29155.1; PID:G159109
A>Note: Sequence extracted from NCBI backbone (NCBI:94071, NCBI:P.94074)
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
C:Keywords: NADP; oxidoreductase
F:135/Binding site: substrate (Lys) #status predicted
```

```
Query Match 48.7%; Score 1324.5; DB 1; Length 449;
Best Local Similarity 58.2%; Pred. No. 1.2e-89;
Matches 260; Conservative 67; Mismatches 111; Indels 9; Gaps 5;

Qy 86 VRQLTETFMKDPDEQEFMQAVREAVVSLQPFVEXKRPBLP--IFKQIYPEREVTFRVSWL 145
Dy 6 IEELIAVIKQRDGHMTFFRQAVEEVVSLKVFIEREKYIPIFERMLEPERVILFRVPM 65
Qy 146 DDAGNLTQVNRGFRVOYSSAIGPYKGLRPHSVNLSTIMKFLAFOIFKNSLTTLPMGGK 205
Dy 66 DDARIVNNGFRVOYSSAIGPYKGLRPHSVNLSTIMKFLAFOIFKNSLTTLPMGGK 125
Qy 206 GGSDFDPKGSDAEVMRFCSFMTELQRHISYVDVPAGDIGVAREIGYLFQGYKRTK 265
Dy 126 GGSDFDPKGSNDENVMRFCSFMTELQRHISYVDVPAGDIGVAREIGYLFQGYKRTK 185
Qy 266 NYTGVLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSGANVAQYCA 325
Dy 186 EFTGVLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSGANVAQYCA 245
Qy 326 ELLLEKGAIVLSLSDSGYVVEPNPFTREQLQAVDMKKKNSARISEYKS--DTAVVY 382
Dy 246 EKLQDAKAVLTFSDSNGTIVDKGFNEBKLAHLMYLNKNGR-GRVSEFKDKYPSVAYYE 304
Qy 383 GDRKPMPE-LDCQVDIAFPKATONEIDEHDAELLKHGGOYVVEGANNPSTNEAIHKYKN 441
Dy 305 G--KKPMEPCFPGQNDICMPCATQNEVSGDDATRLVGLGKFLVAGANNPSTNEAIVHYHA 362
Qy 442 AGIITPCGKAANAGVAVSGLEMTQNRMSLMTREBVDKLRIMKDIYDSAMGPSRRYN 501
Dy 363 KGVAVYCPAKASNNAGVAVSGLEMTQNRMSLMTREBVDKLRIMKDIYDSAMGPSRRYN 422
```

```
Qy 502 --VDLAAGANIAGFTKVAADAVKAQAV 526
Dy 423 HPKNYQMGANIAGFTKVAADSMIEGCV 449
```

## RESULT 3

```
H83072
glutamate dehydrogenase PA4588 (imported) - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83072
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brumadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: H83072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <STO>
A:Cross-references: UNIPROT:Q9HVJ7; GB:AE004872; GB:AE004091; NID:99950829; PIDN:AAG07976
A:Experimental source: strain PA01
C:Genetics:
A:Gene: gdhA; PA4588
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
```

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Query Match 48.1%; Score 1309; DB 2; Length 445;
Best Local Similarity 59.2%; Pred. No. 1.6e-88;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;
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Qy 86 VRQLTETFMKDPDEQEFMQAVREAVVSLQPFVEXKRPBLP--IFKQIYPEREVTFRVSWL 143
Dy 5 VDAFLERLKRDPDQEFMQAVEEVVSLQPFVEXKRPBLP--IFKQIYPEREVTFRVSWL 64
Qy 144 WLDDAGNLTQVNRGFRVOYSSAIGPYKGLRPHSVNLSTIMKFLAFOIFKNSLTTLPMGG 203
Dy 65 WVDQDGRVNRGFRVOYSSAIGPYKGLRPHSVNLSTIMKFLAFOIFKNSLTTLPMGG 124
Qy 204 GGSDFDPKGSDAEVMRFCSFMTELQRHISYVDVPAGDIGVAREIGYLFQGYKRTK 263
Dy 125 GGSDFDPKGSDAEVMRFCSFMTELQRHISYVDVPAGDIGVAREIGYLFQGYKRTK 184
Qy 264 TKQYTGVLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSGANVAQY 323
Dy 185 SNQFTSVLTGKLSYGSSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSGANVAQY 244
Qy 324 CAELLLEKGAIVLSLSDSGYVVEPNPFTREQLQAVDMKKKNSARISEYKSDTAVVY 383
Dy 245 AAKVMEGKQVLSLSDSGYVVEPNPFTREQLQAVDMKKKNSARISEYKSDTAVVY 303
Qy 384 DRRKPMELDCQVDIAFPKATONEIDEHDAELLKHGGOYVVEGANNPSTNEAIHKYKN 443
Dy 304 EGRRPWMLAC--DIAFPKATONEIDEHDAELLKHGGOYVVEGANNPSTNEAIVHYHA 361
Qy 444 IITPCGKAANAGVAVSGLEMTQNRMSLMTREBVDKLRIMKDIYDSAMGPSRRYN 502
Dy 362 ILVAPGASNAGVAVSGLEMTQNRMSLMTREBVDKLRIMKDIYDSAMGPSRRYN 421
Qy 503 DLAAGANIAGFTKVAADAVKAQAV 526
Dy 422 NYKGANIAGFTKVAADAVKAQAV 445
```

## RESULT 4

```
H81050
glutamate dehydrogenase, NADP-specific NMB1710 (imported) - Neisseria meningitidis (strain H81050)
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81050
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
```

ri, H.; Qin, H.; Vamathavan, J.; Gail, J.; Scarlato, V.; Maignani, V.; Pizze, M.  
 Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, E.R.; Rappuoli, R.; V  
 A>Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
 A:Reference number: AB1000; MUID:20175755; PMID:10710307  
 A:Accession: AB1050  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Reads: 1-44 <TET>  
 A:Cross-references: UNIPROT:O9JY71; GB:AE002521; GB:AE002098; NID:g722662; PIDN:AAF4205  
 A:Experimental source: serogroup B, strain MC58  
 C:Genetics:  
 A:Gene: NMB1710  
 C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
 Query Match 47.8% Score 1300.5; DB 2; Length 444;  
 Best Local Similarity 57.4%; Pred. No. 6.9e-88;  
 Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;  
 Qy 85 DVRLITIFMKDPEQGEFMQAVREAVSLDPVEKPELL-PIFKQIYPERVITTRV 142  
 Db 3 DLNTLFAWLKCRNPQEPFHQAVEVFMSLPFLAKPKYTOQSILERIVPERVVRV 62  
 143 SWLDAGNLQVNRGRVYSSAIGYKGLRPHSPVNLSTMKPLAFBQIFKNSLTLLPMG 202  
 Db 63 TWQDDKGVQVNRGRVYSSAIGYKGLRPHSPVNLSTMKPLAFBQIFKNSLTLLPMG 122  
 203 GKGSGDPDPKSGSDAEVNRFCQSPMTLQRIHSYVQDPAGDGVGARIEGYFGQYK 262  
 Db 123 GKGSGSDPDPKSGSDAEVNRFCQAFMTLYNHIGADTDVPAQDGVGARIEGYFGQYK 182  
 Qy 263 ITKNYTVLPEKQGEYSGSEIRPEATGYGAVLPEVNLKDKGESLKGKRLCVSAGVAAQ 322  
 Db 183 IRNEFSSVLTGKGLWCGSLIRPEATGYGCVFAQMLQTRNDSPFGKRVLSIGSGVAAQ 242  
 Qy 323 YCAELLEKGAIVLSLSDSGYVER-NGFTREQLQAVQDMKKKNSRIEYSDRAY 381  
 Db 243 YAAERKALQLGAKVLTVSDNSGFVLPDSDGMEADQALALILEKVRRE-RVATYAKEQGLQ 301  
 Qy 382 VGDRRKPELDCQVDIAFPCATONEIDEHDAELIHKGCQYVVGANPSTNEAIHKYK 441  
 Db 302 YFEKQKPGV-AAEIALPCATONEIDEBAKTLIANCCYVABGANPSTLGAVEQPIK 359  
 Qy 442 AGITYCPGKAAAGVAVSGLEMTQNRMSLWTEBEVYDKLERIMKDIYDSAMGPSRRY- 500  
 Db 360 AGITYAPCKASAGVAVATSGLEMSQNAIRLSMTREBVQRLFGIMQSIHESCL---KYG 415  
 Qy 501 ---NVDLAAGANLAGFTKXADAVKAAQ 524  
 Db 416 KVGDVYVYVNGANLAGFTKXADAVKAAQ 443  
 RESULT 5  
 AB1825  
 glutamate dehydrogenase (NADP) (EC 1.4.1.4) NMA1964 [Imported] - *Neisseria meningitidis*  
 C:Species: *Neisseria meningitidis*  
 C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
 C:Accession: B01825  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 , Holroyd, S.; Jorgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Randsdram,  
 Nature 404, 502-506, 2000  
 A>Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.  
 A:Reference number: AB1775; MUID:20222556; PMID:10761919  
 A:Accession: B01825  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Reads: 1-44 <PAR>  
 A:Cross-references: UNIPROT:O9JY56; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAE8518  
 A:Experimental source: serogroup A, strain 22491  
 C:Genetics:  
 A:Gene: gdhA; NMA1964  
 C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
 A:Keywords: oxidoreductase

Query Match 547.6%; Score 1294.5; DB 2; Length 444;  
Best Local Similarity 57.1%; Pred. No. 1,9e-87;  
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY 85 DVROLLTEIFMKDPEQOEPMQAVREVAVSLQPVFEKRPPELL--PIFKQIVPERVITTRV 142  
DB 3 DLNTLIFANLKQNPNDPEPHQAVEBVFMSLDPLAKNPKYTOGSLERIVPERVVRV 62  
QY 143 SWLDAGNLIQVNRGFRVQYSSAIGPYKGLRFRHPSVNLSTMKPLAFEOIFPKNSLTTLPMG 202  
DB 63 TWODKGGQGVQVNRKGRVQWSSAIGPYKGLRFRHPTVDLGVLFKPLAFQVFNALTTLPMG 122  
QY 203 GKGKSGDPPCKGKSDAEVNRFCOSFMTELORHISYQDVDPAGDIGVAREIGYFPGQYK 262  
DB 123 GKGKSGDPPCKGKSDAEVNRFCQAFMTLRYHIGADTDVAGDIGVGREIGYFPGQYK 182  
QY 263 IYKNYTVGLTPKQEGYSGSEIRPEATGYAVLFEVNLKDKGSLKGRCLVSGAGNVAQ 322  
DB 183 INERSSVLTGKLEWGSILIREATGYGVYPAQANLQTRNDSFEKRVILISGSGNVAQ 242  
QY 323 YCAELLLEKGAIVLSISDSQGYVEP--NGPTRQLOAVODMKKKNSARISEYKSDTVY 381  
DB 243 YAAEKAIQIGAVLTVSDNGFVLPDSCGSEQLALIELKEVRE--RAATYAKEGQLQ 301  
QY 382 VEDRRKPMELDCQVDIAPFCATONIDEHDAELLIKHGCQYVVGAMPSTNEAIIHKYK 441  
DB 302 YFENQKPMGV--AAELALCATONELDEBAKTLNAGCTVVAEGANPSTLGAVEQITK 359  
QY 442 AGIIPCCKAANAGVAVSGLEMTQNRMSLMTREBYRDLERIMQIDYSAMGSPRRY 500  
DB 360 AGILVAPGKASNAAGVATSGLEWSQNAIRLSWTREEVDQGLFGIMQIHESCL---KYG 415  
QY 501 ---NVDLAAGANIAGFTVADAVKAG 524  
DB 416 KVGDTVNVYNGANIAGFVAVDAMLAQG 443

RESULT 6  
A64053  
Glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: A64053  
R:Flitschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirtness, E.F.; Kerlavage, A.; Goeyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodde, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Frazer, C.M.; Smith, H.O.; Venter, A. Article: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A:Reference number: A64000; MUID:95550650; PMID:7542880  
A:Accession: A64053  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-449 <TRIG>  
C:Cross-references: UNIPROT:P43793; GB:U32704; GB:I42023; NID:g1573143; PIDN:AAC21858.1; C:Superfamily: glutamate dehydrogenase (NAD(P)+)  
C:Keywords: NADP; oxidoreductase

Query Match 45.5%; Score 1238; DB 2; Length 449;  
Best Local Similarity 55.6%; Pred. No. 2,8e-53;  
Matches 247; Conservative 64; Mismatches 117; Indels 16; Gaps 5;

QY 90 LTFIMKDEQOEPMQAVREVAVSLQPVFEKRPPELL--PIFKQIVPERVITTRVSWLDD 147  
DB 11 LTKVQRQGYOEFLQAVREFTSIWPLEANPKYRSALLERLVEBERAFQFRVAVTDD 70  
QY 148 AGNLTQVNRGFRVQYSSAIGPYKGLRFRHPSVNLSTMKPLAFEOIFPKNSLTTLPMGCKGK 207  
DB 71 KGVQVYNAFRQFRNSAIGPYKGLRFRHPSVNLSTMKPLAFEOIFPKNSLTTLPMGCKGK 130  
QY 208 SDFPKGSDAEVNRFCOSFMTELORHISYQDVDPAGDIGVAREIGYFPGQYKRTIKNY 267

Db 13 SDPDKGKSDAEVWRFCQALMAELVRHVGADITDVPAGDIIGVGRHEVGLIAYMKKLSNOS 190

Qy 268 TGVLTREKGEYEGSSSELRPEATGYGAVLPIENYVLKXKXGSLKGRCLYSAGANNAYQYAEI 327

Db 191 ACFFETRGISFGGSLILRPBETGGLIYFQALAEKGDSPFGKVVSSGSGENVAQYALIEK 250

Qy 328 LLEKGAIVLSLSDSOGYVVEPNPENGFTREOQAOVQMKKKNNBARISEYKSDPAVYVGRRK 367

Db 251 ALSGAKVYVTCSDSSGVYVDPNPGFTTEKKAALFDI-KYTKRGVXVDVAEQGCIQYFEGGR 309

Qy 388 PWELDCQVDIAPFCALQNETIDEDHAELIKHGCOYVVEGAMPESTNEARIKTKAGIITYC 447

Db 310 PWEEV-QVDIAFPCAQNETIELSDQRIILKXGVKLVAGGAMPPITTEXTALLAADVLFG 367

Qy 448 PGKAAVAGVAVASGLEMTQNRMSLWTRBEEDVKLERIMKIYDSAGMPSRRY----- 500

Db 368 PGKAAVAGVAVASGLEMAQSQRILVYTAEEVDQIHRIMDIHANNC-----KRYOTIEGE 423

Qy 501 NVDLAAGANTAGCTTAYDAVYKAG 524

Db 424 NINYYVGANVAGFVYVADAMLAQG 447

QY	DB	Score	DB 2	Length	Gaps
QY	10487	44.7%	1214.5	444	4
QY	glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola				
C/Species:	Prevotella ruminicola				
C/Date:	16-Jul-1999 #sequence_revision:16-Jul-1999 #text_change:09-Jul-2004				
C/Accession:	T10487				
R/Name:	Z.T.: Morrison, M.				
	submitted to the EMBL Data Library, December 1996				
A/Reference number:	Z17049				
A/Accession:	T10487				
A/Status:	preliminary; translated from GB/EMBL/DBJ				
A/Molecule type:	DNA				
A/Residues:	1-444 <MEN>				
A/Cross-references:	UNIPROT:P95544; EMBL:U82240; NID:g1772844; PID:g1772845				
A/Experimental source:	strain B14				
C/Genetics:					
A/Note:	gdnA				
C/Superfamily:	glutamate dehydrogenase (NAD(P)+)				
C/Keywords:	NADP; oxidoreductase				
Query Match	44.7% Score 1214.5; DB 2; Length 444;				
Best Local Similarity	54.9% Pred. No. 1.5e-81;				
Matches	242; Conservative 73; Mismatches 119; Indels 7; Gaps 4;				
QY	88	QLTLEIFKEDDEOEFMOAVEVANAASLPVEKRPET--LPIFKOIVEPERVITFRVSWL	145		
DB	5	EVIEKTKAKKPGQPEYIQAQSVGLCTIGTBEEYVKNKHPFEKAMILERTLCVPDRILQRFVSWV	64		
QY	146	DDAGNLQVNRGPRVOYSSAIGPYKGLAFHFSYNISSIMKPLAFQIFKNSLTLLPMGGSK	205		
DB	65	DDNNVQVNTLDLRYVOHNAIIPYKGLGFPHKSVNASSILKPLAFBQTFKNSLTLLPMGGAK	124		
QY	206	GGSPFDPKGSKDAEWMRFCSQFMTELOHISYVOPVPAGDVGVARREICGYFGQYKRTTK	265		
DB	125	GGSPFDPKGSKDMEMRFCSQAFMELTYLLIGPDEVPVAGDVGVARREICGYFGQYKRLTH	184		
QY	266	NYTGVLPKGOEYGGSEIRPEATGYAVLFEYENLKDGGSLKGRCLVSGAGNVAOYCA	325		
DB	185	QFGILTKGHEFGGSLIRPEATGYGVNYFLIEDMLKTRGESLEGKTVLVSGGNVAOYTI	244		
QY	326	ELLEKGAIVLSLSQGVYEPNGFTBQLOAVDDMKKNNASRISEYKSDTAVYVUDR	385		
DB	245	EKLQIQAKPPTCSSNSGYIYDPPDIDAEKLAFLIMELKNVNR--GRIKIYAEKRYGVKYEN	303		
QY	386	RKPEMLDCOVNIAFPACATONEIDEADALLKGGCOYVVEGANMPSSTAEALHKYKAGII	445		
DB	304	ARPW--GKKALITATCATODEINEAKTLLIANGVPAVSEGANMPTPEALIKVPODAKIL	361		
QY	446	YCPGKANAGVAASGLEMTQNRMSLNTTREVVRDKLERIMKDIYDSAM--GPSRRVND	503		

Db 362 YCPGASNAGGVAITSLEMSQNSEKLSMTREVDTKLHNIMDEIHANCVKYGTPEPGYIN 421

QY 504 LAAGNINFTTKVADAVKAQG 524  
|||:||||| ||| : |||

Db 422 YVKGANVAGFMKVKACAMMAQG 442

RESULT 8  
 D98019  
 glutamate dehydrogenase (NADP) (EC 1.4.1.4) [imported] - Streptococcus pneumoniae (Strair  
 C|Species: Streptococcus pneumoniae  
 C|Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #ext\_change 09-Jul-2004  
 C|Accession: D98019  
 R|Hoeking, J.A.; Albom Jr., W.; Arnold, J.; Blassczak, L.; Burett, S.; Dehoff, B.S.; De  
 e, R.; LeBlanc, D.J.; Lee, L.N.; Letkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc  
 y, P.; Sun, P.M.; Winkler, M.E.  
 Y. Bacteriol. 183, 5709-5717, 2001  
 A|Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
 A|Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
 A|Reference number: A97872; MUID:21429245; PMID:11544234  
 A|Accession: D98019  
 A|Status: preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-448 <KUR>  
 A|Cross-references: UNIPROT:O8DPG0; GB:AE007317; PID:AAK9984.L; PID:G1545813; GSPDB:GN  
 C|Genetics:  
 A|Gene: gdhA  
 C|Superfamily: glutamate dehydrogenase (NAD(P)+)  
 C|Keywords: oxidoreductase

Query Match	Similarity	Score	DB 2:	Length	448:
Beef Local	55.7%	Pred. No. 1.6e-81;			
Matches	248;	Conservative	62;	Mismatches	127;
				Indels	8;
				Gaps	4;
QY	86	VRQLLTLEFMKDPDEOEFMQAVREAVNSLOPVEKESPELL--IFKQIVERVRYTRVS	143		
Db	8	IQSVETVYKARNGHEAEFLQAVBEFNTLEPVEKHPYEENILARITEPERVYSFRVP	67		
QY	144	WDDNGNLOVNGFRVQVSSAIGPYKGIIRFHSVNLSTMKFLAFEOIFKNSLTTLEMG	203		
Db	68	WVDRDGKTVQVNNGYRVQFNSAVGPRYGGIRFHPVNAQGLIKFLGFEOIFKNVLTGLPIG	127		
QY	204	GKGSDFDPKGSDAVWARFCOSFMTELORHIEYVDVPAGDIGVAREIGYLFQYKRI	263		
Db	128	GKGSDFDPKGTIDAEVWARFCOSFMTELQKHIPSIDVPAGDIGVAREIGYLYGQYKRL	187		
QY	264	TKNYTGVLTPKQOEGSEIRPEATGYAVLFEVENVLKDKGESLKGRCLVSGAGNAVQY	323		
Db	188	NQFDAGVLTGKPLGCGSLIRPEATGYGLVYVEEMLKANGNSFAGKRVVISGGNAVQY	247		
QY	324	CAELLLEKGAIVLSDSGQVYVEPENGFTREQQAVODMKKNNSARISEYKSTAVYVG	383		
Db	248	ALQKATELGATVIVSDSNGVYIDENG--DFDLIVDAEKRR-AHLTEYAAEKATATY	303		
QY	384	DRRKEWELDCQVDIAFPFCATONEIDEHDAELLKHGCOVYVEGANGPSTINEAHLKYNK	443		
Db	304	HEGSWYTAAGNVDIALLPCATONEINEGAARKLVAQCVICSEGANPNSNDALKVYENG	363		
QY	444	IYYCGKAANAGGAVVSGLEMTQNRMSLWMTREEVDPKLERIKMDIYDSAMGSRRYNV	502		
Db	364	IFYGPAKKAANAGGAVVSALEMSQNSLRLSMTREEVDPGRUKDITMNTFNIAKTSSEYGLD	423		
QY	503	-DLAAGANAGFTKVAADAVKAGAV	526		
Db	424	KDYLAGANIATAFENVANAMIAQIV	448		

RESULT 9

H95151

NADP-specific glutamate dehydrogenase [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae

C/Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004

C/Accession: H95151



R;Teteljin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Hickam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,  
neon, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Lofcus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A.; Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: H95151  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-448 <KIR>  
A:Cross-references: UNIPROT:Q97QB4; GB:AE005672; PIDN:AAK75409.1; PID:G14972791; GSPDB:G  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SPJ306  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 44.6%; Score 1212; DB 2; Length 448;  
Best Local Similarity 55.5%; Pred. No. 2.3e-81;  
Matches 247; Conservative 63; Mismatches 127; Indels 8; Gaps 4;

QY 86 VROLTELFMDPEQEFMOAVREAVASLOVPEKRPBLP--IFKQIVBERVITFRVS 143  
DB 8 IQSVETVYKANGHEAEFLQAVEEFNLTBEVFEKHPEYIEENTLARIITEPERVVSFRVP 67  
QY 144 WLDDAGNLQVNRGRVVOSSAIGYKGGIRFHPSPVNSIMKFLAPEQIFKNSLTTLPMGC 203  
DB 68 WVDGDKIQVNRGRVVOSSAIGYKGGIRFHPSPVNSIMKFLAPEQIFKNSLTTLPMGC 127  
QY 204 GKGSGDFDPKGSDAEYVRFQSFMTLORHISYVODPADIGVAREIGYLFQGYKRI 263  
DB 128 GKGSGDFDPKGSDAEYVRFQSFMTLORHISYVODPADIGVAREIGYLFQGYKRI 187  
QY 264 TKATYGVLTPEKQSGSEIRPEATGYAVLPVENVLKDKGSLKGRCLVSGAGVAY 323  
DB 188 NQPDAGVLTPEKQSGSEIRPEATGYAVLPVENVLKDKGSLKGRCLVSGAGVAY 247  
QY 324 CAELLEKGAIVLSLSDQGYVEPNQTRBQLQAVQDMKKNSARISEKSDPAVYVG 383  
DB 248 ALQVATELGATVISVSDNGVYIDENGL--DPLLVAVKERR-ARLTTEAAKATATY 303  
QY 384 DRKRPWELDCQVDIAFCATONEIDEHDAELLIKGCOYVEGANMPESTNEAIHKYNAG 443  
DB 304 HEGVWVYTAGNYDIALPCATONEINGEAKRLVAGVYCVSEGANMPSDDAIKYKENG 363  
QY 444 IYCPGAAAGVAVSGLMONTORMSIMWTRREVRDLERIMKIDYSAMGPSRRYV- 502  
DB 364 IFYGPAAAGVAVSGLMONTORMSIMWTRREVRDLERIMKIDYSAMGPSRRYV- 423  
QY 503 -DLAAGNINAGFTTVADAVKAGAV 526  
DB 424 KDYLAGNINAGFTTVADAVKAGAV 448

## RESULT 10

E83912  
NADP-specific glutamate dehydrogenase gdhA [imported] - *Bacillus halodurans* (strain C-12)

C:Species: *Bacillus halodurans*  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: E83912  
R:Takami, H.; Nakaseko, K.; Takaki, Y.; Maeno, G.; Saeaki, R.; Masui, N.; Fuji, F.; Hirz  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: E83912  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-458 <STO>  
A:Cross-references: UNIPROT:Q9RB34; GB:AF001514; GB:BA000004; NID:G10174613; PIDN:BA0058  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: gdhA  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 44.5%; Score 1210.5; DB 2; Length 458;  
Best Local Similarity 54.7%; Pred. No. 3e-81;  
Matches 252; Conservative 71; Mismatches 121; Indels 17; Gaps 7;

QY 77 LVHGKINPDVROLTEIF---MKDPQOEFMOAVREAVASLOVPEKRPBLP--PIFKQ 130  
DB 4 LVREKQYVDVQYVQHYETVYKRNPNHEFHQAVKEVPDLSLPLVLIKHYQVYQALLER 63  
QY 131 IVEPERVITFRVSWLDDAGNLQVNRGRVVOSSAIGYKGGIRFHPSPVNSIMKFLAPEQ 190  
DB 64 IVEPERVITFRVSWLDDAGNLQVNRGRVVOSSAIGYKGGIRFHPSPVNSIMKFLAPEQ 123  
QY 191 IFKNSLTTLPMGSGSGSDPDKGSDAEYVRFQSFMTLORHISYVODPADIGVAREIGY 250  
DB 124 IFKNSLTTLPMGSGSGSDPDKGSDAEYVRFQSFMTLORHISYVODPADIGVAREIGY 183  
QY 251 REIGYLFQGYKRIKNT--TGVLTPKGOEYSGSEIRPEATGYAVLPVENVLKDKGSLK 309  
DB 184 KEIGYMFQYKRIKNT--TGVLTPKGOEYSGSEIRPEATGYAVLPVENVLKDKGSLK 243  
QY 310 KRCIVSGAGVAYQCAELLEKGAIVLSLSDQGYVEPNQTRBQLQAVQDMKKNSA 369  
DB 244 STVYVSGAGVAYQCAELLEKGAIVLSLSDQGYVEPNQTRBQLQAVQDMKKNSA 299  
QY 370 RISRYKSD--TAVYVGRRRPWLDCQVDIAFCATONEIDEHDAELLIKGCOYVEGA 427  
DB 300 RISRYKSD--TAVYVGRRRPWLDCQVDIAFCATONEIDEHDAELLIKGCOYVEGA 357  
QY 428 NMPESTNEAIHKYNAGIYCPGAAAGVAVSGLMONTORMSIMWTRREVRDLERIMK 487  
DB 358 NMPESTNEAIHKYNAGIYCPGAAAGVAVSGLMONTORMSIMWTRREVRDLERIMK 417  
QY 488 DIYDSAMGPSRRYV--DLAAGNINAGFTTVADAVKAGAV 526  
DB 418 NIYRESIKABLYEASGNLVAGNINAGFTTVADAMISHGV 458

## RESULT 11

E75362  
glutamate dehydrogenase - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: E75362  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; i  
s.; Shen, M.; Yamachev, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: E75362  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-424 <WHI>  
A:Cross-references: UNIPROT:Q9RTN9; GB:AE002013; GB:AE000513; NID:G6459484; PIDN:AAI1275  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR1718  
A:Map position: 1  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 44.3%; Score 1205.5; DB 2; Length 424;  
Best Local Similarity 56.2%; Pred. No. 6.3e-81;  
Matches 240; Conservative 61; Mismatches 119; Indels 7; Gaps 4;

QY 104 MQAVREAVASLOVPEKRPBLP--PIFKQIVBERVITFRVSWLDDAGNLQVNRGRVVOY 161  
DB 1 MQAVREAVASLOVPEKRPBLP--PIFKQIVBERVITFRVSWLDDAGNLQVNRGRVVOY 60  
QY 162 SSAIGYKGGIRFHPSPVNSIMKFLAPEQIFKNSLTTLPMGSGSGSDPDKGSDAEYV 221  
DB 61 SSAIGYKGGIRFHPSPVNSIMKFLAPEQIFKNSLTTLPMGSGSGSDPDKGSDAEYV 120

Oy	222	RECOSEFMTELORHISYVODVPAGDIGVAPBETIGLFGQYKXITKNTYGVLTPIKQOEYGS	281
Db	121	RFQOMLTELNRHJGPRDTPVPAQDIGVGRVETVGLAGMMKLANHAGVFTGKLSYGS	180
Oy	282	EIREPATGYAVLFEVENVLKDKGESLKGRKCLVSGAGNVAOYCAELLLEKGAIVLSLDS	341
Db	181	LLREBPATGYGVYFEVHEHLRDOQRMEMELRVSYSVSGSNGVAIATEKALHGAHVLTSMS	240
Oy	342	OGYVYEPBPGFREDLOAVODMKKKNSARISEYSSDPAVVYVGBRKKPMELDCCOVDIAPC	401
Db	241	GGYVDEBGFYYDKLAVLMDIKNERR-GRVADYAREVGAERPGVRHR--DVPDVALPC	297
Oy	402	ATONEIDEHDAELLKHGCOYVEGANNPSTNEAIHKYNKAIIYCPGKAAANGVAVSG	461
Db	298	ATONEHGDADDARTTIAGGVRVVAEGANPCCLLAIOAFEEAGYVYAPGKATNAGGVAATSG	357
Oy	462	LEMTONRMSLWMTREEVARDKLERIMKDIYDSAMGSPSR--YNVVLAAGANIAGFTYKADA	519
Db	358	LEMSONMORLSMTREEVORLRSITMSAIHDBCLTEYGRPRDHNHVSYLDSGANIAGVVKATA	417
Oy	520	VKAQCAV 526	
Db	418	MREQVL 424	

```

RESULT 12
DEBCEM
glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Escherichia coli (strain K-12)
N:Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C:Species: Escherichia coli
C:Date: 03-Aug-1984 #sequence revision 20-Sep-1984 #text_change 09-Jul-2004
C:Accession: A00382; A22413; A64936
R:McPherson, M.J.; Wootton, J.C.
Nucleic Acids Res. 11, 5257-5266, 1983
A:Title: Complete nucleotide sequence of the Escherichia coli gdhA gene.
A:Reference number: A00382; MUID:83272967; PMID:6308576
A:Accession: A00382
A:Molecule type: DNA
A:Residues: 1-447 <MCP>
A:Cross-references: UNIPROT:P00370; GB:X00988; GB:U01615; GB:K00565; NID:G41543; PIDN:CAAC74831.1; PID:G1788059;
R:Vallee, F.; Becerril, B.; Chen, E.; Seeburg, P.; Heyneker, H.; Bolivar, F.
Gene 27, 193-199, 1984
A:Title: Complete nucleotide sequence of the glutamate dehydrogenase gene from Escherichia coli
A:Reference number: A22413; MUID:84209849; PMID:6373501
A:Accession: A22413
A:Molecule type: DNA
A:Residues: 1-447 <VAL>
A:Experimental source: strain K12
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen,
A.; Rose, D.U.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A64936
A:Strain: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-447 <BLAT>
A:Cross-references: GB:A000271; GB:U00096; NID:G1788058; PIDN:AACT4831.1; PID:G1788059;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: gdhA
A:Map position: 27 min
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
R:Keywords: homohexamer; NADP; oxidoreductase
A:Binding site: substrate (lys) #status predicted
A:Binding site: substrate (lys) #status predicted

```

[illegible]

```

OY 144 HUDDAGNLOVNRGPRVOYSSATIPRYKGLRPFHSVNLSTIMKPLAFEDIFKNSLTLLPMGG 203
Db 67 WDDDNQOQVNNAMRVQFSSAIGPYKGMRFHPSVNLSTIKELFGEOTFNALTTLLPMGG 126
OY 204 GKGSDFPBGKSDAEVNRFCOSFMTELORHISVYODVPAGDIGVGRREIGYLFQYKRI 263
Db 127 GKGSDFPBGKGSBEGRVNRFCQALMTELYRHLGADTDVPAGDIGVGRREIGVPMGMKKL 186
OY 264 TKNYTGVLTPKGOEYGSERIRPEATGYGAVLFEVENVLKDGESLKGRCILVSGAGNVAQY 323
Db 187 SNNTACVFEFGKSLIFEGSGLIRPEATGYGLVFEYFEAMLKRGHMGFEGRVRSVSGSAGNVAQY 246
OY 324 CAELLLEKGAIVLSLSDSGYVYEPNGFTREDOQAVQDMKKNNNSAISEYKSDTAVYVG 383
Db 247 ALEKMEFARVITASDSSGTAVDESGETFEKKEKARLIEI-KASRDGQVADVAEFGVLYL 305
OY 384 DRRKFMELDCQVDIAPPCATONEIDEDHAEILLKHGCOQYVEGANNPSTBEAIIHKYNKAG 443
Db 306 EGQGMSL--PDIALLPCATONELDVDAHQHOLIANGVKAIEGANNPTTIEATELLPQOG 363
OY 444 IIPCQKANNAGVAVSGLEMTONRMSLNMWTRBEVDKLERIMKDIYDSAM--GPSRRY 500
Db 364 VLFARQKANNAGVATSGLEMAQNAARLQMKQAEKVADRLHIMLDIHACVYEHGSEGEQT 423
OY 501 NVDLAAGANIAGFTKYADAVKAQAGAV 526
Db 424 N--VYQGANIAGFVKVADMLAQVI 447

```

RESULT 13  
 P96990  
 NADP-specific glutamate dehydrogenase [imported] - Clostridium acetobutylicum  
 C|Species: Clostridium acetobutylicum  
 C|Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C|Accession: P96990  
 R|Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A|Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium  
 A|Reference number: A96900; MUID:21359325; PMID:21359325  
 A|Accession: P96990  
 A|Status: preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-443 **UNR-**  
 A|Cross-references: UNIPROT:Q97L29; GB:AE001437; PIDN:AAK78713.1; PID:gl5023619; GSPDB:GN  
 A|Experimental source: Clostridium acetobutylicum ATCC824  
 C|Genetics:  
 A|Gene: CAC0737  
 C|Superfamily: glutamate dehydrogenase (NAD (P) +)

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Query Match Similarity      44.1%; Score 1199; DB 2; Length 443;
Best Local Similarity      54.4%; Pred. No. 2e-80;
Matches 242; Conservative 69; Mismatches 122; Indels 12; Gaps 5;

QY      86  VROLTLEIFMKDPEQOEFMQAVREAVNSLQPEKEPELT--EIFKQIVEPERVITERS 143
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      4  LKHVMDVDYIKRNPNEPEFHQAVKEVLTSLIYAEKKPEWMKDIPIKIVEPERQIRVP 63
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

QY      144 WDDNGNLQVNRGFRVQYSSAIGPYKGRFRHFSVNLSTMKFLAFEDIFKNSLTTLPMGC 203
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      64  WDDNGEBEIRINKGFPIQFNSAIGPYKGRFRHFSVNLGIYKFLGFEDIFKNSLTGLPIGC 123
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

QY      204 GKGSQSDPDKGSDAEVWMEFCQSPMTELORHISYVDVPADGIGVGRREIGYLFQGVKRI 263
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      124 GKGSQSDPEFKSSNSIIRKFCQSPMLLENKYITGANTDVDPAGDIGVGRREIGYLYGMKKRI 183
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

QY      264 TKNYGVLTLPKQOEVGSGSEIRPEATGYGAVLPEVNTLKDKGESLKGKRCIVSGAGNVAOY 323
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      184 RNESTGVLTKKGLTLGGSLVREATGYGCLYFNNEMLKKAKGKSPDGAITVLISSGNVAIY 243
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

QY      324 CAELLLEKGAIVLSSDQGYVEPENGFTREQLQAVQDMKKKNSARISYKS--DTAAVY 381
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

```

Db 244 ANOKATOLGAKVAMSDSNGYIYDANGINLTIKRIKVERK---RIHEXTKHPNASY 299  
Qy 382 VGDRRKPMELDCQVDIAFPCATONEIDEHDAELIKHGCOYVVEGANMSTNEAIHKNK 441  
Db 300 TEGCDGIMKLC--DIALPCATONEIDENSAKTLIANGCAVAGGANNPSTTEVADLEIK 357  
Qy 442 AGIIPCAGKANAGVAVSGLEMTQNRMSLMTREBEVDKLERIMKDIYDSAMGSPSRRYN 501  
Db 358 NKVIFGPAKANAGVAVSALEMSONSRMTREBEVDTKQNMKIKYICSNAAENY 417  
Qy 502 VD--LAAGANTAGFTKVADAVKAG 524  
Db 418 FEDNLVAGANTAGFTKVAAEAMYSIG 442

## RESULT 14

C90937  
NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: C90937  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hatlori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: C90937  
A:Status: preliminary  
A:Statue: preliminary  
A:Molecule type: DNA  
A:Residues: 1-447 <HAV>  
A:Cross-references: UNIPROT:O8XDM9; GB:BA000007; PTDN:BA835890.1; PID:G13361934; GSPDB:C  
A:Experimental source: strain O157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: Ec2467  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 44.0%; Score 1198; DB 2; Length 447;  
Best Local Similarity 53.8%; Pred. No. 2.4e-80;  
Matches 240; Conservative 68; Mismatches 128; Indels 10; Gaps 5;  
Qy 86 VRQLTEIFMKDPQOEFMQAVREAVNSLQVPEKREL--LPFKQIVBERVITRRVS 143  
Db 7 LESFLNHVQKRDPMQTEFAQVREVMWTLMPLEQNPYKQMSLLERLVEBERVIOFRVV 66  
Qy 144 WLDDAGNLQVNRGRVVOYSSAIGPYKGLRFPSPVNSIMKFLAFBQIFKNSLTLLPMG 203  
Db 67 WDDRNQVQVNRKRVOPSSAIGPYKGMFRHPSVNSILKFLGFEBQTFKALTTLLPMG 126  
Qy 204 GKGSDPDPKGSDAEYVRCQSFMTLOHISVQVDPADIGVAREIGYLFQYKRI 263  
Db 127 GKGSDPDPKGSSEGEVWRCQALMTLEYRHLGADTDVPADIGVAREIGVFMAGMKKL 186  
Qy 264 TKNTYGLTPKGEYGESEIRPEATGYAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 323  
Db 187 SNTNACVFTKGLSGFGLIRPEATGYGLVFTFEMLKRGHMGEGKRVSVSSGNAQY 246  
Qy 324 CAELLLEKGAIVLSLSDSGYVVEPNQFTREOLQAVODMKKNNASRISEKSDTAVYV 383  
Db 247 AIEKAMEFGARVITASDSGTVVDESGETTEKARLEI--KSSRDGRVADYAKFGLVYL 305  
Qy 384 DRKPMELDCQVDIAFPCATONEIDEHDAELIKHGCOYVVEGANMSTNEAIHKNKAG 443  
Db 306 EGQOPMSV--PVDIALPCATONEIDVDAHQLIANGVAVAGANMPTTEATELFOQAG 363  
Qy 444 IIVCGKAANAGVAVSGLEMTQNRMSLMTREBEVDKLERIMKDIYDSAM--GPSRRY 500  
Db 364 VLPAPGKAANAGVAVSGLEMTQNRMSLMTREBEVDKLERIMKDIYDSAM--GPSRRY 500  
Qy 501 NVDLAAGANTAGFTKVADAVKAGAV 526  
Db 424 N--YVQGANITAGFTKVADAVKAGAV 526

RESULT 15  
G85785  
NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: G85785  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: G85785  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-447 <STO>  
A:Cross-references: UNIPROT:O8XDM9; GB:AE005174; NID:G12515786; PIDN:AA656747.1; GSPDB:C  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: gdhA  
C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 44.0%; Score 1198; DB 2; Length 447;  
Best Local Similarity 53.8%; Pred. No. 2.4e-80;  
Matches 240; Conservative 68; Mismatches 128; Indels 10; Gaps 5;  
Qy 86 VRQLTEIFMKDPQOEFMQAVREAVNSLQVPEKREL--LPFKQIVBERVITRRVS 143  
Db 7 LESFLNHVQKRDPMQTEFAQVREVMWTLMPLEQNPYKQMSLLERLVEBERVIOFRVV 66  
Qy 144 WLDDAGNLQVNRGRVVOYSSAIGPYKGLRFPSPVNSIMKFLAFBQIFKNSLTLLPMG 203  
Db 67 WDDRNQVQVNRKRVOPSSAIGPYKGMFRHPSVNSILKFLGFEBQTFKALTTLLPMG 126  
Qy 204 GKGSDPDPKGSDAEYVRCQSFMTLOHISVQVDPADIGVAREIGYLFQYKRI 263  
Db 127 GKGSDPDPKGSSEGEVWRCQALMTLEYRHLGADTDVPADIGVAREIGVFMAGMKKL 186  
Qy 264 TKNTYGLTPKGEYGESEIRPEATGYAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 323  
Db 187 SNTNACVFTKGLSGFGLIRPEATGYGLVFTFEMLKRGHMGEGKRVSVSSGNAQY 246  
Qy 324 CAELLLEKGAIVLSLSDSGYVVEPNQFTREOLQAVODMKKNNASRISEKSDTAVYV 383  
Db 247 AIEKAMEFGARVITASDSGTVVDESGETTEKARLEI--KSSRDGRVADYAKFGLVYL 305  
Qy 384 DRKPMELDCQVDIAFPCATONEIDEHDAELIKHGCOYVVEGANMSTNEAIHKNKAG 443  
Db 306 EGQOPMSV--PVDIALPCATONEIDVDAHQLIANGVAVAGANMPTTEATELFOQAG 363  
Qy 444 IIVCGKAANAGVAVSGLEMTQNRMSLMTREBEVDKLERIMKDIYDSAM--GPSRRY 500  
Db 364 VLPAPGKAANAGVAVSGLEMTQNRMSLMTREBEVDKLERIMKDIYDSAM--GPSRRY 500  
Qy 501 NVDLAAGANTAGFTKVADAVKAGAV 526  
Db 424 N--YVQGANITAGFTKVADAVKAGAV 526

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Job time : 43 sec

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: July 9, 2005, 18:24:52 ; Search time 181 Seconds  
(without alignments)  
1488.142 Million cell updates/sec

Title: US-10-627-886-2  
Perfect score: 2720  
Sequence: 1 MGTALVAKPTVAPLAPRR.....GANIAGFTKVADAVKAGAV 526

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2488.5	91.5	523	1	DHE4_CHLSO
2	1375	50.6	510	2	081LF7
3	1361	50.0	1203	2	07RQ39
4	1328	48.8	446	2	07Y2U9
5	1327.5	48.8	449	2	07R3N7
6	1324.5	48.7	449	1	DHE4_GILMA
7	1309	48.1	445	2	09HVT7
8	1300.5	47.8	444	2	08U771
9	1294.5	47.6	444	2	09JTS6
10	1287.5	47.3	449	2	088Q23
11	1286.5	47.3	470	2	096940
12	1286.5	47.3	470	2	081LR0
13	1285	47.2	445	2	0923C4
14	1284.5	47.2	437	2	07Y2U7
15	1265	46.5	442	2	09TXS8
16	1264	46.5	442	2	09GTX5
17	1257	46.2	465	2	06S143
18	1253.5	46.1	536	2	07RG75
19	1250.5	46.0	448	2	08G6L0
20	1250.5	46.0	445	2	08G6L0
21	1249.5	45.9	447	2	08FDE7
22	1241.5	45.6	448	2	08XK85
23	1240.5	45.6	449	2	08E4J6
24	1239.5	45.6	448	2	0835G2
25	1238	45.5	449	1	DHE4_HAEIN
26	1236.5	45.5	449	2	08DY77
27	1234	45.4	447	2	061083
28	1231.5	45.3	462	2	06SW57
29	1230.5	45.2	449	2	08DUZ2
30	1230	45.2	449	2	09CPJ4
31	1225.5	45.1	444	1	DHE3_BACIN

32	1225	45.0	448	2	09AIW1	09AIW1 streptococc
33	1214.5	44.7	444	1	DHE4_PRRU	P95544 streptococc
34	1214	44.6	448	2	08DPG0	08DPG0 streptococc
35	1212	44.6	448	2	097QB4	097QB4 streptococc
36	1210.5	44.5	458	2	09KB34	09KB34 bacillus ha
37	1206.5	44.4	447	2	07VSN6	07VSN6 bordetella
38	1205.5	44.3	424	2	09RTN9	09RTN9 deinococcus
39	1205.5	44.3	444	2	064O81	064O81 bacteroides
40	1205.5	44.3	464	2	07WU7	07WU7 bordetella
41	1202	44.2	448	2	08BXN9	08BXN9 lactobacill
42	1201	44.2	447	1	DHE4_ECOLI	P00370 escherichia
43	1200.5	44.1	446	2	060996	060996 trypanosoma
44	1200	44.1	449	2	06AJB1	06AJB1 desulfofocale
45	1199	44.1	443	2	097L29	097L29 clostridium

## ALIGNMENTS

RESULT 1  
DHE4\_CHLSO STANDARD; PRT; 523 AA.  
ID DHE4\_CHLSO  
AC P28998;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 29-MAR-2004 (Rel. 43, Last annotation update)  
DE NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH)  
DE (Fragment).  
OS Chlorobacterium chlorobacterium.  
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;  
OC Chlorellaceae; Chlorella.  
OX NCBI\_TaxID=3076;  
RN [1]  
RP MEDLINE=92032762; PubMed=1718478;  
RA Cook J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.;  
RT "A nuclear gene with many introns encoding ammonium-inducible  
chloroplast NADP-specific glutamate dehydrogenase(s) in Chlorella  
sorokiniana";  
RT Plant Mol. Biol. 17:1023-1044(1991).  
CC -1- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate  
+ NH(3) + NADPH.  
CC -1- SUBUNIT: Homo- and heterohexamers of alpha and beta subunits. Both  
subunits are encoded by the same gene.  
CC -1- SUBCELLULAR LOCATION: Chloroplast.  
CC -1- INDUCTION: By ammonium.  
CC -1- PPM: The N-termini of the alpha and the beta chains are blocked.  
CC -1- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)  
or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
DR EMBL; X58832; CA41636.1; -;  
DR EMBL; X58831; CA41635.1; ALT\_SEQ.  
DR PIR; S17949; S17949.  
DR HSP; P24295; IADP.  
DR InterPro; IPR006095; GLFV\_dehydrog.  
DR InterPro; IPR006096; GLFV\_dehydrog.C.  
DR InterPro; IPR006097; GLFV\_dehydrog.N.  
DR Pfam; PF00208; GLFV\_dehydrog.1.  
DR Pfam; PF002812; GLFV\_dehydrog.N.1.  
DR PRINTS; PR00082; GLFV\_DEHYDROGENASE.  
DR PROSITE; PS00074; GLFV\_DEHYDROGENASE; 1.  
DR Chloroplast; NADP; Oxidoreductase.  
KW NON TER  
FT AC SITE 202 202 By similarity.  
FT SITE 523 AA; 57529 MM; A35FE730B5FE7974 CRC64;  
SQ SEQUENCE

Query Match 91.5%; Score 2488.5; DB 1; Length 523;  
 Best Local Similarity 95.7%; Pred. No. 2e-161;  
 Matches 488; Conservative 4; Mismatches 13; Indels 5; Gaps 2;

QY 17 ARPPCLAPWPCAMVRSARADYRAVAVSLLEBQISAMDITGDTMLQCAVQOMATKAGTEG 76  
 DB 19 ALPRAVA---CARGRSAKRVDYAAK--RLRSRSPMDATGTGDTMLQCAVQOMATKAGTEG 73  
 QY 77 LVHGIKNPDRVQLLTETFMKDPQEQQEPMQAVREAVSLQPFEGREPELLPIFKQIVPER 136  
 DB 74 LVHGIKNPDRVQLLTETFMKDPQEQQEPMQAVREAVSLQPFEGREPELLPIFKQIVPER 133  
 QY 137 VITFRVSWLDAGNLQVNRGFRVQSSAIGPYKGLRPHSPVNSIMKFLAFEQIFKNSL 196  
 DB 134 VITFRVSWLDAGNLQVNRGFRVQSSAIGPYKGLRPHSPVNSIMKFLAFEQIFKNSL 193  
 QY 197 TITLPMGGKGSDDPDKGSAEYMRFCQSPMTLQRIHSYVQVPAQDVGARREIGYL 256  
 DB 194 TITLPMGGKGSDDPDKGSAEYMRFCQSPMTLQRIHSYVQVPAQDVGARREIGYL 253  
 QY 257 FGQYKRLTKNYTGVLTFRKGOEYGSSEIRPEATGYAVLFVENVLKDGESLKGRCCLVSG 316  
 DB 254 FGQYKRLTKNYTGVLTFRKGOEYGSSEIRPEATGYAVLFVENVLKDGESLKGRCCLVSG 313  
 QY 317 AGNVAQYCAELLLEKGAIVLSLSDSGYVVEPNCFTRERQLQAVQDMKKNNASARISEYKS 376  
 DB 314 AGNVAQYCAELLLEKGAIVLSLSDSGYVVEPNCFTRERQLQAVQDMKKNNASARISEYKS 373  
 QY 377 DTAVYVDRRRPWLDDQVDFAPCATONEIDEHDAELLIKHGQYVVEGANMSTTEAI 436  
 DB 374 DTAVYVDRRRPWLDDQVDFAPCATONEIDEHDAELLIKHGQYVVEGANMSTTEAI 433  
 QY 437 HKYKAGIITCPGNAAGVAVSGLEMTQNRMSLNTREEVDRKLERIMKDIYDSAMGP 496  
 DB 434 HKYKAGIITCPGNAAGVAVSGLEMTQNRMSLNTREEVDRKLERIMKDIYDSAMGP 493  
 QY 497 SRRYVNDLAAGANIAGFTKYADAVKAGAV 526  
 DB 494 SREYVNDLAAGANIAGFTKYADAVKAGAV 523

RESULT 2  
 Q8ILF7 PRELIMINARY; PRT; 510 AA.  
 AC Q8ILF7;  
 DT 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Glutamate dehydrogenase, putative.  
 GN ORFNames=PF14\_0286;  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;  
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,  
 RA Carlton J.M., Pain A., Nelson K.E., Bowman K.E., Paulsen I.T., James K.,  
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kye S.,  
 RA Chan M.S., Nene V., Shalimov S.J., Suh B., Peterson J., Angiuoli S.,  
 RA Perlea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,  
 RA Martin D.M., Fairclark A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,  
 RA McPhaden G.I., Cummings L.M., Subramanian G.M., Mungall C.,  
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
 RA Frazer C.M., Barrell B.,  
 RT "Genome sequence of the human malaria parasite Plasmodium  
 RT falciparum.";  
 RL Nature 419:498-511(2002).  
 DR EMBL; AE014820; AAN36899.1; -  
 DR HSSP; P24295; IAUJ.  
 DR GO; GO:0016491; P:oxidoreductase activity; IEA.  
 DR GO; GO:0006520; P:amino acid metabolism; IEA.  
 DR InterPro; IPR006095; GUFV\_denydrog.

DR InterPro; IPR006096; GUFV\_denydrog\_C.  
 DR InterPro; IPR006097; GUFV\_denydrog\_N.  
 DR Pfam; PF00208; GUFV\_denydrog\_1.  
 DR Pfam; PF02812; GUFV\_denydrog\_N; 1.  
 DR PRINTS; PR00082; GUFV\_denydrog\_N.  
 DR PROSITE; PS00074; GUFV\_denydrog\_N; 1.  
 SQ SEQUENCE 510 AA; 57343 MW; AC400045297AC64F CRC64;

Query Match 50.6%; Score 1375; DB 2; Length 510;  
 Best Local Similarity 60.0%; Pred. No. 2e-85;  
 Matches 267; Conservative 66; Mismatches 104; Indels 8; Gaps 5;

QY 86 VROLLEIFMKDPEQQEPMQAVREAVSLQPFEGREPELLPIFKQIVPERVITFRVSWL 145  
 DB 70 IEELREKVVSKNKPBEFLQAFEEVLSCLKPFKKNVYIGVLENIAPERPVIQFRVPMI 129  
 QY 146 DDAGNLQVNRGFRVQSSAIGPYKGLRPHSPVNSIMKFLAFEQIFKNSLTLTPMGCGK 205  
 DB 130 NDKGEHMKNGFRVQVNSVIGPYKGLRPHSPVNSIMKFLAFEQIFKNSLTLTPMGCGK 189  
 QY 206 GGSDFDPKGSDAEYMRFCQSPMTLQRIHSYVQVPAQDVGARREIGYLFGQYKRLTK 265  
 DB 190 GGSDFDPKGSDAEYMRFCQSPMTLQRIHSYVQVPAQDVGARREIGYLFGQYKRLTK 249  
 QY 266 NYTGVLTFRKGOEYGSSEIRPEATGYAVLFVENVLKDGESLKGRCCLVSGAGNVAQYCA 325  
 DB 250 NYTGVLTFRKGOEYGSSEIRPEATGYAVLFVENVLKDGESLKGRCCLVSGAGNVAQYCA 309  
 QY 326 ELLLEKGAIVLSLSDSGYVVEPNCFTRERQLQAVQDMKKNNASARISEY--KSDTAVYV 383  
 DB 310 ELLLEKGAIVLSLSDSGYVVEPNCFTRERQLQAVQDMKKNNASARISEY--KSDTAVYV 367  
 QY 384 DRKRPWLDDQVDFAPCATONEIDEHDAELLIKHGQYVVEGANMSTTEAIHKYKAG 443  
 DB 368 ENQKPNIP--DIAPCATONEINERDADLFQNKCMAVEGANMPTIKALHKQNN 425  
 QY 444 IIVCPKNAAGVAVSGLEMTQNRMSLNTREEVDRKLERIMKDIYDSAMGPSRRY--N 501  
 DB 426 IIVCPKNAAGVAVSGLEMTQNRMSLNTREEVDRKLERIMKDIYDSAMGPSRRY--N 485  
 QY 502 VDLAAGANIAGFTKYADAVKAGAV 526  
 DB 486 SDLVAGANIAGFTKYADAVKAGAV 510

RESULT 3  
 Q7RQ39 PRELIMINARY; PRT; 1203 AA.  
 AC Q7RQ39;  
 DT 01-MAR-2004 (TReMBLrel. 26, Created)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Glutamate dehydrogenase.  
 GN Name=PY01264;  
 OS Plasmodium yoelii yoelii.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=73239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=17XN1;  
 RC PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Koo J.T.W., Perlea M.,  
 RA Salva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
 RA Shalimov S.J., van Aken S.B., Riedmiller S.B., Feldblyum T.V.,  
 RA Cho U.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,  
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Frazer C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.,  
 RT "Genome sequence and comparative analysis of the model rodent malaria  
 RT parasite Plasmodium yoelii yoelii.";



RL Mature 419:512-519 (2002).  
CC CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
DR EMBL: AAB0100331; EAA20557.1; -  
DR HSSP: P24295; IADP.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro: IPR005135; Exo\_endo\_phos.  
DR InterPro: IPR006095; GLFV\_dehydrog.  
DR InterPro: IPR006096; GLFV\_dehydrog\_C.  
DR InterPro: IPR06097; GLFV\_dehydrog\_N.  
DR Pfam: PF03372; Exo\_endo\_phos; 1.  
DR Pfam: PF02008; GLFV\_dehydrog; 1.  
DR Pfam: PF02812; GLFV\_dehydrog\_N; 1.  
DR PRINTS: PR00082; GLFV\_DEHYDROGENASE.  
DR PROSITE: PS00074; GLFV\_DEHYDROGENASE; 1.  
SQ SEQUENCE 1203 AA; 13909 MW; DBE1988BD4C21715 CRC64;  
  
Query Match 50.0%; Score 1361; DB 2; Length 1203;  
Best Local Similarity 59.3%; Pred. No. 5.5e-84;  
Matches 264; Conservative 65; Mismatches 108; Indels 8; Gaps 5;  
  
QY 86 VRQLTEIFMKDPQOEPMQAVREAVSLQPVFEKRPPELLPIFKQIVPERVITFRVSWL 145  
DB 763 IEEKENAVISKNDQHEFLQAFEEVLTSLKVPFKKIIYLGLVNISEPREVIGFRVPMI 822  
QY 146 DDAGNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFQIFKNSLTLLPMGGG 205  
DB 823 NDNGEHKINGFRVQYSSVGLPYKGLRPHPTVNLSTVKFGEQIFKNSLTLLPMGGG 882  
QY 206 GGSDFDPKSKSDAEVNRFCQSFMTLQRIHSYQDVPAQDVGAREIGVFGQYKRTK 265  
DB 883 GGSDFDPKSKSENEILRFCSFMDNLRVYIGPNTDIPAGDVGVSREIGVFGYKRLKN 942  
QY 266 NYTGVLTPKQOYEGSEIRPEATGYAVLFEVENVLKDKGSLKGRCLVSGAGNVAQYCA 325  
DB 943 KFESEVLGKINIKMGSGNIRSEATGYAVAFENMLSDMBESLNKKTICVSSGNAQYLV 1002  
QY 326 ELLLEKGAIVLSDSQGYVEPNQFTREQLQAVQDMKKKNSARISEY--KSDTAVYV 383  
DB 1003 EKLLEKAKVLTWSDSGYLIEPNGFTREQLKDIEMIKNVRK-RIKEYLKYSTAKFF- 1060  
QY 384 DRRKPMELDCQVDIAFPCATONEIDEHDAELLIKHGCQYVEGANMSTNEAIHKYKAG 443  
DB 1061 ENERPMAVPC-DIVFPCATONEITENDADLLINCKCLVEGANMPTNKKAMKLEKNK 1118  
QY 444 ILYCPGKAANAGVAVGLEMTQNRMSLNTREBVDKLERIMKDIYDSAMGSPRRY--N 501  
DB 1119 ILICPSGAANAGVAVGLEMTQNRMSLNTREBVDKLERIMKDIYDSAMGSPRRY--N 501  
QY 502 VDLAAGANIAGFTKVADAVKAGAV 526  
DB 1179 TDLVAGANVAGFTKVADSVFEGGL 1203  
  
RESULT 4  
Q7YZU9 PRELIMINARY; PRT; 446 AA.  
AC Q7YZU9; (TREMBLrel. 25, Created)  
DT 01-MAR-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Glutamate dehydrogenase (Fragment).  
DS Name=gdh;  
OS Spirochaete bacterium.  
OC Eukaryota; Diplomonadida; Hexamitidae; Hexamitinae; Spirochaete.  
OX NCBI\_TaxID=103874;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 50380;  
RX PubMed=12820901; DOI=10.1186/1471-2148-3-14;  
RA Anderson J.O., Roger A.J.;

RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene  
transfer within and between prokaryotes and eukaryotes."  
RL BMC Evol. Biol. 3:14-14 (2003).  
DR EMBL: AF533884; AAP83851.1; -  
DR HSSP: P24295; IADP.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro: IPR006095; GLFV\_dehydrog.  
DR InterPro: IPR006096; GLFV\_dehydrog\_C.  
DR InterPro: IPR06097; GLFV\_dehydrog\_N.  
DR Pfam: PF02008; GLFV\_dehydrog; 1.  
DR Pfam: PF02812; GLFV\_dehydrog\_N; 1.  
DR PROSITE: PS00074; GLFV\_DEHYDROGENASE; 1.  
FT NON TER 1  
SQ SEQUENCE 446 AA; 49309 MW; AEB4D2A1762DB80 CRC64;  
  
Query Match 48.8%; Score 1328; DB 2; Length 446;  
Best Local Similarity 58.6%; Pred. No. 2.7e-82;  
Matches 262; Conservative 65; Mismatches 110; Indels 10; Gaps 6;  
  
QY 85 DVKQLTEIFMKDPQOEPMQAVREAVSLQPVFEKRPPELLPIFKQIVPERVITFRVSW 144  
DB 5 DLKXVLLQO--RDANHIEFQAVNEVSLTVFEEENPKYISVEQLLEBERVIMFRVPM 61  
QY 145 LDPAQNLQVNRGFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFQIFKNSLTLLPMGGG 204  
DB 62 TDDKGEVNIKRGVQYNSLIGPYKGLRPHPSVNLSTMKFLAFQIFKNSLTLLPMGGG 121  
QY 205 KGSDFDPKSKSDAEVNRFCQSFMTLQRIHSYQDVPAQDVGAREIGVFGQYKRTK 264  
DB 122 KGSDFDPKSKSNGEVNRFCQSFMTLSRIHQFTDVPADIDVGAREIGVFGQYKRTK 181  
QY 265 KNTYGVLTPEKQOYEGSEIRPEATGYAVLFEVENVLKDKGSLKGRCLVSGAGNVAQY 324  
DB 182 NQFGLITGKAVYSGSLIRPEATGYAVYVLEMMNDNDIDKGVLLSGAGNVAQY 241  
QY 325 AELLLEKGAIVLSDSQGYVEPNQFTREQLQAVQDMKKKNSARISEY--KSDTAVYV 382  
DB 242 TEKLIHGAIPLSDSNGTILIEPNGFTREQLKDIEMIKNVRK-GRISBTSSSTAKY 300  
QY 383 GDRKPMELDCQVDIAFPCATONEIDEHDAELLIKHGCQYVEGANMSTNEAIHKYKAG 441  
DB 301 -BGRPMAVYEGKVDVIMPCATONEVNGTEAEVYKGLAVYSGAGNVAQY 359  
QY 442 AGIYCPGKAANAGVAVGLEMTQNRMSLNTREBVDKLERIMKDIYDSAMGSPRRY--N 501  
DB 360 SKVEYGPAKASNAGVAVTSGLEMTQNRMSLNTREBVDKLERIMKDIYDSAMGSPRRY--N 501  
QY 502 V--DLAAGANIAGFTKVADAVKAGAV 526  
DB 420 KKGNYQGANVAGFTKVADSMIDQCV 446  
  
RESULT 5  
Q7R3N7 PRELIMINARY; PRT; 449 AA.  
AC Q7R3N7; (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DE GIP 39 39379 38030.  
OS Giardia lamblia ATCC 50803.  
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
OX NCBI\_TaxID=184922;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WB C6;  
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
RT "Draft sequence of the Giardia lamblia genome."  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

```

CC preliminary data.
DR EMBL: AACB01000014; FAA41919.1; -.
DR HSSP: P24295; 1AUP.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006520; P:amino acid metabolism; IEA.
DR InterPro: IPR006095; GLFV_dehydrog.
DR InterPro: IPR006096; GLFV_dehydrog_C.
DR InterPro: IPR006097; GLFV_dehydrog_N.
DR Pfam: PF00208; GLFV_dehydrog_N.1.
DR Pfam: PF02812; GLFV_dehydrog_N.1.
DR PRINTS: PR00082; GLFV_DEHYDROGENASE.1.
DR PROSITE: PS00074; GLFV_DEHYDROGENASE.1.
DR SEQUENCE 449 AA; 49734 MW; 2397B34BEBBCAEE2 CRC64;

Query Match 48.8%; Score 1327.5; DB 2; Length 449;
Best Local Similarity 58.4%; Pred. No. 2.9e-82;
Matches 261; Conservative 66; Mismatches 111; Indels 9; Gaps 5;

QY 86 VRQLTEIFMKDEQOEPMQAVREAVSLQPFVEKREPELLPIFKQIPEPRVITFRVSWL 145
DB 6 IEELIATIVIKORDGHTMFROAVEVDSLKVIFEREKTIPIFERMLEPERRVITFRVPM 65
QY 146 DDAGNLQVNRGFRVQYNSAIGPYKGLRFRHPSVNLSTMKFLAFEQIFKNSLTLLPMGGGK 205
DB 66 DDAGRINVRNGFRVQYNSALGPYKGLRFRHPSVNLSTIKFLGFEQILKNSLTLLPMGGGK 125
QY 206 GGSDFDPKGSDAEVRMFCOSFMTELQRHSYQDVDPAGDIGVAREIGYLFQGYKRIK 265
DB 126 GGSDFDPKGSDEVRMFCOSFMTELQRHVADTDVPAIGVAREIGYLFQGYKRLRN 185
QY 266 NYTGVLTPKQOEGYSEIRPEATGYAVLFVENYLDKSGSLKGRCLVSGAGNVAQYCA 325
DB 186 EFTGVLTGKNVKNMGSGFIRPEATGYAVLFLEMKCDNNVTIRKQVTLSSGSNVAQFAC 245
QY 326 ELLLEKGAIVLSLDSQGYVEPNFTREQLQAVQDMKKKNSARISEYKS--DTAVYV 382
DB 246 EKLIQIGAKVLTSSDSNGITVDKGFNEEKLAMLYKNEKR-GRVSEFDKXPVAVYVE 304
QY 383 GDRRKPE-LDCCVDIAFPQATONEIDEHDAELLIKGCOYVVGAMPSSTNEAIIHYNK 441
DB 305 G--KKPWECEEGQVDCIMPCATQNEVSGDDKTRVLVGLKFLVAGAMPSTAEVHYHA 362
QY 442 AGIIYCPGKANAGVAVSGLEMTQNMSLMNTREEVRLKLERIMKDIYDSAMGPSRRYN 501
DB 363 KGVWYGPARKSNAGVSVSGLEMSQNSVRLQMTAEVDQKLRGIMRGIFVACRDTAKYG 422
QY 502 --VDLAAGANIAGFTKVAADVAKQAV 526
DB 423 HPKNYQMGANIAGFLKVDMSMIEGCV 449

RESULT 6
DHE4_GIALA STANDARD; PRT; 449 AA.
ID DHE4_GIALA
AC P28724; Q24961;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH) (NADP-dependent glutamate dehydrogenase).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiae; Giardia.
OC NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=92218410; PubMed=1559991;
RA Yee J., Dennis P.P.;
RT "Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene from the primitive eucaryote Giardia lamblia.";
RL J. Biol. Chem. 267:7539-7544(1992).
RX MEDLINE=96155200; PubMed=8587793;

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RA Montis P.T., Mayrhofer G., Andrews R.H., Homan W.L., Limper L.,
RA By P.L.;
RT "Molecular genetic analysis of Giardia intestinalis isolates at the
RT glutamate dehydrogenase locus.";
RL Parasitology 112:1-12(1996).
CC -1- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate
CC + NH(3) + NADPH.
CC -1- SUBUNIT: Homohexamer (By similarity).
CC -1- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M84604; AAA29155.1; -.
DR EMBL: U47632; AAB05400.1; -.
DR PIR: A42489; A42489.
DR HSSP: P24295; 1AUP.
DR InterPro: IPR006095; GLFV_dehydrog.
DR InterPro: IPR006096; GLFV_dehydrog_C.
DR InterPro: IPR006097; GLFV_dehydrog_N.
DR Pfam: PF00208; GLFV_dehydrog_N.1.
DR Pfam: PF02812; GLFV_dehydrog_N.1.
DR PRINTS: PR00082; GLFV_DEHYDROGENASE.
DR PROSITE: PS00074; GLFV_DEHYDROGENASE.1.
KW NADP; Oxidoreductase.
FT ACT_SITE 125 125 By similarity.
FT CONFLICT 249 249 I -> L (in Ref. 2).
SQ SEQUENCE 449 AA; 49766 MW; 5497B35209B549F6 CRC64;

Query Match 48.7%; Score 1324.5; DB 1; Length 449;
Best Local Similarity 58.2%; Pred. No. 4.7e-82;
Matches 260; Conservative 67; Mismatches 111; Indels 9; Gaps 5;

QY 86 VRQLTEIFMKDEQOEPMQAVREAVSLQPFVEKREPELLPIFKQIPEPRVITFRVSWL 145
DB 6 IEELIATIVIKORDGHTMFROAVEVDSLKVIFEREKTIPIFERMLEPERRVITFRVPM 65
QY 146 DDAGNLQVNRGFRVQYNSAIGPYKGLRFRHPSVNLSTMKFLAFEQIFKNSLTLLPMGGGK 205
DB 66 DDAGRINVRNGFRVQYNSALGPYKGLRFRHPSVNLSTIKFLGFEQILKNSLTLLPMGGGK 125
QY 206 GGSDFDPKGSDAEVRMFCOSFMTELQRHSYQDVDPAGDIGVAREIGYLFQGYKRIK 265
DB 126 GGSDFDPKGSDEVRMFCOSFMTELQRHVADTDVPAIGVAREIGYLFQGYKRLRN 185
QY 266 NYTGVLTPKQOEGYSEIRPEATGYAVLFVENYLDKSGSLKGRCLVSGAGNVAQYCA 325
DB 186 EFTGVLTGKNVKNMGSGFIRPEATGYAVLFLEMKCDNNVTIRKQVTLSSGSNVAQFAC 245
QY 326 ELLLEKGAIVLSLDSQGYVEPNFTREQLQAVQDMKKKNSARISEYKS--DTAVYV 382
DB 246 EKLIQIGAKVLTSSDSNGITVDKGFNEEKLAMLYKNEKR-GRVSEFDKXPVAVYVE 304
QY 383 GDRRKPE-LDCCVDIAFPQATONEIDEHDAELLIKGCOYVVGAMPSSTNEAIIHYNK 441
DB 305 G--KKPWECEEGQVDCIMPCATQNEVSGDDKTRVLVGLKFLVAGAMPSTAEVHYHA 362
QY 442 AGIIYCPGKANAGVAVSGLEMTQNMSLMNTREEVRLKLERIMKDIYDSAMGPSRRYN 501
DB 363 KGVWYGPARKSNAGVSVSGLEMSQNSVRLQMTAEVDQKLRGIMRGIFVACRDTAKYG 422
QY 502 --VDLAAGANIAGFTKVAADVAKQAV 526
DB 423 HPKNYQMGANIAGFLKVDMSMIEGCV 449

RESULT 7
Q9HVJ7

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ID 09HVJ7 PRELIMINARY; PRT; 445 AA.  
AC 09HVJ7;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Glutamate dehydrogenase.  
GN Name=gda; OrderedLocusNames=PA4588;  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
NCBI\_TaxID=287;  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=ATCC 15692 / PAOI;  
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;  
RA Stever C.K., Phan X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,  
Garber R.L., Goltzy L., Tolentino E., Westbrook-Madman S., Yuan Y.,  
Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,  
Smith K.A., Spencer D.H., Wong G.K.-S., Mu Z., Paulsen I.T.,  
Reizer J., Slier M.H., Hancock R.E.W., Lory S., Olson M.V.,  
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an  
RT opportunistic pathogen."  
RL Nature 406:959-964(2000).  
DR EMBL; AE004872; AAC07976.1; -  
DR PIR; H81072; H81072.  
DR HSSP; P24295; IAUP.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro; IPR006095; GLFV\_dehydrog.  
DR InterPro; IPR006096; GLFV\_dehydrog\_C.  
DR InterPro; IPR006097; GLFV\_dehydrog\_N.  
DR Pfam; PF00208; GLFV\_dehydrog\_1.  
DR Pfam; PF02812; GLFV\_dehydrog\_N; 1.  
DR PRINTS; PR00082; GLFDHGNASE.  
DR PROSITE; PS00074; GLFV\_DEHYDROGENASE; 1.  
DR Complete proteome.  
SQ SEQUENCE 445 AA; 48856 MW; 643EB12BC84F3418 CRC64;  
Query Match 48.1%; Score 1309; DB 2; Length 445;  
Best Local Similarity 59.2%; Pred. No. 5.3e-81;  
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;  
QY 86 VROLTEIFMKDPEQOEFOAVREVAVSLQVFEKREPLL--TFKQVPERVITPRV 143  
DB 5 VDAFLERKRBDPOEFHQAVEEVLKSLWPFLEANPHYLAGIIEIVEBERAILEFRVP 64  
QY 144 WLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFEOIFKNSLTLLPMG 203  
DB 65 WVDQGRVVRVGRVQKSSAIGPYKGLRPHPSVNLQVLFKFLAFEOYFKNSLTLLPMG 124  
QY 204 GKGSGDFDPKGSDAEVRFCQSFMTLQRHISYQDVDPADIGVAREIGYFGQYKR 263  
DB 125 GKGSGDFDPKGSDAEVRFCQSFMTLQRHISYQDVDPADIGVAREIGYFGQYKR 184  
QY 264 TKNYTVLTPRGQYSGSEIRPEATGYAVLFVENVLKDGESLKGKRLVSGAGNVAQ 323  
DB 185 SNQTSVLTGKGLSYGSLRPEATGFCYVFAQEMLKDRGRGFDGQVVAISGSGNVAQ 244  
QY 324 CAELLLEKGAIVLSLDSQGYVEEPNGFTREOLAVQDMKKKNSARISEKSDTAAYV 383  
DB 245 AARKVMEMGKIVLSLDSQGYVEEPNGFTREOLAVQDMKKKNSARISEKSDTAAYV 303  
QY 384 DRRKRWELDCQVDIAFPQATQNEIDEHDAELLIKHGCQYVVGAMPSGTNEAIHKYNK 443  
DB 304 EGRPWPGLAC--DIALPCATQNEIDAEADARLLANGCVAEGANMPSLTBAVDLEAG 361  
QY 444 ILYPRGKAANGAIVASGLETONRMSLNTWRETRDGLERIMDYDIA-MGSRKRV 502  
DB 362 ILYPRGKAANGAIVASGLETONRMSLNTWRETRDGLERIMDYDIA-MGSRKRV 421  
QY 503 DLAAGANIAGFTKADAVKAGAV 526

DB 422 NYVGANIAGFVKVADMLAGV 445  
RESULT 8  
ID 09YV71 PRELIMINARY; PRT; 444 AA.  
AC 09YV71;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Glutamate dehydrogenase, NADP-specific.  
GN OrderedLocusNames=NM1710;  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
NCBI\_TaxID=491;  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B;  
RX MEDLINE=2015755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;  
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,  
Neison K.B., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,  
Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,  
Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,  
Dougherty B.A., Mason T.M., Clecko A., Parksey D.S., Blair E.,  
Citlome H., Clark E.B., Cotton M.D., Urtreback T.R., Khouri H.M.,  
Qin H., Vamathavan U.J., Gill J., Scarlato V., Maignani V., Pizzo M.,  
Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,  
RA Venter J.C.;  
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
RT MC58."  
RL Science 287:1809-1815(2000).  
DR EMBL; AE002521; AAF42057.1; -  
DR PIR; H81050; H81050.  
DR HSSP; P24295; IAUP.  
DR TIGR; NM1710; -  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro; IPR006095; GLFV\_dehydrog.  
DR InterPro; IPR006096; GLFV\_dehydrog\_C.  
DR InterPro; IPR006097; GLFV\_dehydrog\_N.  
DR Pfam; PF00208; GLFV\_dehydrog\_1.  
DR Pfam; PF02812; GLFV\_dehydrog\_N; 1.  
DR PRINTS; PR00082; GLFDHGNASE.  
DR PROSITE; PS00074; GLFV\_DEHYDROGENASE; 1.  
DR Complete proteome.  
SQ SEQUENCE 444 AA; 48490 MW; 8B2CFCA89EF7DAF CRC64;  
Query Match 47.8%; Score 1300.5; DB 2; Length 444;  
Best Local Similarity 57.4%; Pred. No. 2e-80;  
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;  
QY 85 DVROLTEIFMKDPEQOEFOAVREVAVSLQVFEKREPLL--PIFKQVPERVITPRV 142  
DB 3 DNLTFANLQKRNPNQEPFHQAVEVMSLDPLAKRPXTQSLRIEVEBERVAVRV 62  
QY 143 SWDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFEOIFKNSLTLLPMG 202  
DB 63 TWQDDKQOVVNRGVRVQKSSAIGPYKGLRPHPTVDLGVLFKFLAFEOYFKNALTTLLPMG 122  
QY 203 GKGSGDFDPKGSDAEVRFCQSFMTLQRHISYQDVDPADIGVAREIGYFGQYKR 262  
DB 123 GKGSGDFDPKGSDAEVRFCQSFMTLQRHISYQDVDPADIGVAREIGYFGQYKR 182  
QY 263 IYKNTVLTLPKQGYSGSEIRPEATGYAVLFVENVLKDGESLKGKRLVSGAGNVAQ 322  
DB 183 IRNEFSVLTGKGLSEMGSLRPEATGYCVAQAMLTQRNDSFEKRVLISSGNVAQ 242  
QY 323 YCAELLLEKGAIVLSLDSQGYVEEP-NGFTREOLAVQDMKKKNSARISEKSDTAAY 381  
DB 243 YAAEKAIQLAKVLTVSDSNGFVLFPDSGMTAQLAALIELKEVRR-RVATYAKEGLQ 301  
QY 382 VGDRKRWELDCQVDIAFPQATQNEIDEHDAELLIKHGCQYVVGAMPSGTNEAIHKYNK 441

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Db 302 YFEKQKPMGV--AAEIALPCATQNELDEBAKTLILANGCYVAGGAMPSTLGAVEQFIK 359
Qy 442 AGIYCPGKANAGVAVSGLEMTQNRMSLMTREEVYDKLERIMKDIYSGAMPSSRY- 500
Db 360 AGIYAPGKASNAGVAVTSGLEMSQNAIRLSMTREEVDRFLFGIMQSIHESCL---KYG 415
Qy 501 ----NVDLAGANIAGFTKVAADAVKAQG 524
Db 416 KVGDVTVMYVNGANIAGFVKVADAMLAQG 443

RESULT 9
Q9UT56 PRELIMINARY; PRT; 444 AA.
AC Q9UT56;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Glutamate dehydrogenase (EC 1.4.1.4).
GN Name=gdhA; OrderedlocusNames=NMA1964;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Cauchemez C.M.,
RA Klee S.R., Morelli G., Baaham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moulie S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
DR EMBL; AL162757; CAB85184.1; -.
DR PIR; B81825; B81825.
DR HSSP; P24295; IADP.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006095; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFV_DEHYDROGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGNASE; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 444 AA; 48462 MW; DEFLA7BBDDEF424 CRC64;

Query Match 47.6%; Score 1294.5; DB 2; Length 444;
Best Local Similarity 57.1%; Pred. No. 51e-80;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

Qy 85 DVROLLTEIFMKDPOQEFMOAVREAVSLQVPEKRELLP--IFKQIYPERVITFRV 142
Db 3 DLNLTFLANLKQKRNPOEFHQVAVEVMSLDPLAKMPKTYQOSILBERTIYPERVIFRV 62
Qy 143 SWLDAGNLQVNRGRPVYSSAIGPYKGLRPHPSVNLISIKFLAFEOIFPKSLITLTPMG 202
Db 63 TWODDKGVQVNRGRPVYSSAIGPYKGLRPHPSVNLISIKFLAFEOIFPKSLITLTPMG 122
Qy 203 GKGSGSDFDPKSKDAEVMRQCQSPMTELQHSIVYDVPAGDIGVAREIGYLFQGYKR 262
Db 123 GKGSGSDFDPKSKDAEVMRQCQSPMTELQHSIVYDVPAGDIGVAREIGYLFQGYKR 182
Qy 263 ITKRYTGYLTPKQGYGSGSEIRPEATYGVANLFEVBNVLKDGESLKGKRCVSGAGNVAQ 322
Db 183 IRNFSFVLTGKGLGEMGSLIRPEATYGVYFAQAMLTQTNDSPEGRKVLISGSGNVAQ 242
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Qy 323 YCAELLLEKCAIVLSLDSQGYIYEP-NGFTREQLQAVQDMKKNSARISEKSDTAVY 361
Db 243 YAAEKAIQIGAKVLTYSDSNGFVLPDSGMSBAQLAALIELKEVRE-RVATYAKEQGLQ 301
Qy 382 VGDPRKMEVDCQVDIAFPATQNEIDEDHAEILLIKGCGIYVVGANMPSTNAIHKYK 441
Db 302 YFEKQKPMGV--AAEIALPCATQNELDEBAKTLILANGCYVAGGAMPSTLGAVEQFIK 359
Qy 442 AGIYCPGKANAGVAVSGLEMTQNRMSLMTREEVYDKLERIMKDIYSGAMPSSRY- 500
Db 360 AGIYAPGKASNAGVAVTSGLEMSQNAIRLSMTREEVDRFLFGIMQSIHESCL---KYG 415
Qy 501 ----NVDLAGANIAGFTKVAADAVKAQG 524
Db 416 KVGDVTVMYVNGANIAGFVKVADAMLAQG 443

RESULT 10
Q88Q23 PRELIMINARY; PRT; 449 AA.
AC Q88Q23;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=gdhA; OrderedlocusNames=PP0675;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22433060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzaple E.K., Scanlan D., Tran K.,
RA Moazzar A., Ulteback T.R., Rizzo M., Lee K., Koback D., Moestl D.,
RA Wedler H., Lauber J., Steppandic D., Hobeisel J., Straetz M., Helm S.,
RA Kewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tremmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AE016776; AAN6300.1; -.
DR HSSP; P24295; IADP.
DR TIGR; PP0675; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006095; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFV_DEHYDROGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGNASE; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 48871 MW; EPI733B6ABC89627 CRC64;

Query Match 47.3%; Score 1287.5; DB 2; Length 449;
Best Local Similarity 58.2%; Pred. No. 1.6e-79;
Matches 259; Conservative 55; Mismatches 124; Indels 7; Gaps 4;

Qy 86 VRÖLLTEIFMKDPOQEFMOAVREAVSLQVPEKRELLP--IFKQIYPERVITFRV 143
Db 8 VDFNFLAKQKRDQGOEFHQVAVEVLTLPFLEAPNPHYQOSILBERTIYPERVIFRV 67
Qy 144 SWLDAGNLQVNRGRPVYSSAIGPYKGLRPHPSVNLISIKFLAFEOIFPKSLITLTPMG 203
Db 68 WVDQGVQVNRGRPVYSSAIGPYKGLRPHPSVNLISIKFLAFEOIFPKSLITLTPMG 127
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0Y 204 GKGGSDPFPKGSDBEWNMFQCSFMELOGRHSIYODVAGDGVGABEIGYFGGYKRI 263
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 128 GKGGSDPFPKGSDBEWNMFQCFAMFSELVRHIGADCDVPAGDGVGABEIGFNFQYKRL 187
0Y 264 TKNYGVGLTPKGOEYVGSSEIRPEATGYAVLFVEYNVLKDGESLKGKRCIVSAGNVAOY 323
    :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 188 ANQFISVLTKGMTYGGSLIRPEATYGCYVFAEBMLKRODKRI DGRRAVSSGNAOY 247
0Y 324 CAELLLEKGAIVLISDSQGYVYEPNFTREQLQAVODMKKKNNSARISEYKSDTVVYVG 383
    :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 248 AARKMDLGGKVIISLDSSEGTLYAEBGLDQADQALMELKNVNR -GRISLAAQOFGLEFR 306
0Y 394 DRKPEWELDCQVDIAFPCCATONEIDEHDBELLKHGCOYVVEGAMPSTNEALHKNYKAG 443
    :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 307 KGOTPMSLPC--DIALPCATONELGAEADARTLLRNCGICVAEGANPPTLEAVDIFLDAG 364
0Y 444 IITYCGKAANAGGVAVSGLEMTONRHSLSMTREEVPDKLERIKMDIYDSAM--GPSRRYN 501
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 365 ILVYAGKASMNAGGVAVSGLEMSQNRMLMTAGEVDSKLHNIMQSIIHACVHGEEADGR 424
0Y 502 VDLAAGANIAGFTKVAADVAKAGAV 526
Db 425 INYVKGANIAGFVKVADAMLAQGV 449

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ID	Accession	Source	Score	DB 1	DB 2	Length	Gaps
0696940	PRELIMINARY;	PRT;	470	AA.			
AC	096940;						
DT	01-MAY-1999	(TREMBLrel, 10, Created)					
DT	01-MAY-1999	(TREMBLrel, 10, Last sequence update)					
DE	05-JUL-2004	(TREMBLrel, 27, Last annotation update)					
DE	Glutamate dehydrogenase (NADP+)	(EC 1.4.1.4).					
GN	Name=GDH; Synonyms=GDH;						
OS	Plasmodium falciparum.						
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.						
OX	NCBI_TaxID=5833;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=99089647; PubMed=9874251;						
RA	Wagner J.T., Luedemann H., Faerber P.M., Lottspeich F.,						
RA	Krauch-Siegel R.L.;						
RT	"Glutamate dehydrogenase, the marker protein of Plasmodium falciparum,						
RT	Cloning, expression and characterization of the malarial enzyme.";						
RL	Eur. J. Biochem. 258:813-819(1998).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RA	Li L.H., Li M., Wu Y.S., Wang P.;						
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; Y12927; CAA73390.1; -.						
DR	EMBL; AY040586; AAK77969.1; -.						
DR	HSSP; P24295; IADP.						
DR	GO; GO:0004354; P:glutamate dehydrogenase (NADP+) activity; IEA.						
DR	GO; GO:0016493; P:oxidoreductase activity; IEA.						
DR	GO; GO:0006520; P:amino acid metabolism; IEA.						
DR	InterPro; IPR006095; GLFV_dehydrog.						
DR	InterPro; IPR006097; GLFV_dehydrog_C.						
DR	InterPro; IPR006097; GLFV_dehydrog_N.						
DR	Pfam; PF00208; GLFV_dehydrog_1.						
DR	Pfam; PF02812; GLFV_dehydrog_N; 1.						
DR	PRINTS; PR00082; GLFDHGNASE.						
DR	PROSITE; PS00074; GLFV_DEHYDROGNASE; 1.						
KW	Oxidoreductase.						
SQ	SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;						
Query Match	47.3%;	Score 1286.5;	DB 2;	Length 470;			
Best Local Similarity	55.2%;	Pred. No. 1.9e-79;					
Matches 266;	Conservative 64;	Mismatches 133;	Indels 19;	Gaps 7			
QY	48 ISAMDATTGDFPALQCAVYKQMATKAGTEGLVHGIKIPDVQQLTEIFMKDPEQGFQVAV 107						
DB	1 MSALDKDKGRFVVLDK-----NASYVESLV----DOENNNYVERVWKLDPNQVETLQAF 50						

[illegible]

RESULT 12	PRELIMINARY:	PRT:	470 AA.
OSLIT0			
ID 08LIT0			
AC 08LIT0;			
DT 01-MAR-2003 (TREMBLrel. 23, Created)			
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE NADP-specific glutamate dehydrogenase.			
GN ORFNames=PF14_0164;			
OS Plasmodium falciparum (Isolate 3D7).			
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX NCBI_TaxId=36329;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;			
RA Gardner M.J., Hall N., Fung E., White O., Brittan M., Hyman R.W.,			
RA Carlton J.M., Pahn A., Nelson K.E., Bowman S., Paulsen I.T., James K.,			
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyte S.,			
RA Chan M.S., Nene V., Shallow S.J., Sub B., Peterson J., Angioli S.,			
RA Pereira M., Allen J., Selengut J., Haft D., Mather M.W., Ralph A.B.,			
RA Martin D.M., Fallis A.H., Fraumholz M.J., Roos D.S., Ralph S.A.,			
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,			
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,			
RA Frazer C.M., Barrall B.;			
RT "Genome sequence of the human malaria parasite Plasmodium			
RT falciparum."			
RL Nature 419:498-511(2002).			
DR EMBL; AE014818; AAN36776.1; -.			
DR HSSP; P24295; IAUU.			
DR GO; GO:0016491; F:oxidoreductase activity; IEA.			
DR GO; GO:0006520; P:amino acid metabolism; IEA.			
DR InterPro; IPR006095; GLFV_dehydrog.			
DR InterPro; IPR006097; GLFV_dehydrog_C.			
DR Pfam; PF00208; GLFV_dehydrog_N.			
DR Pfam; PF02812; GLFV_dehydrog_N. 1.			
DR PRINTS; PR00082; GLFDHGNASE			
DR PROSITE; PS00074; GLFV_DEHYDROENASE. 1.			
SEQ SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;			

Query Match 47.3%; Score 1286.5; DB 2; Length 470;  
Best Local Similarity 55.2%; Pred. No. 1.9e-79;  
Matches 266; Conservative 64; Mismatches 133; Indels 19; Gaps 7;  
QY 48 ISMDATGCTALQKAVKQMATAGTGLVHGKNDVROLTEIMKDPQOEPMQAV 107  
DB 1 MSAAKDTGTRVVDK-----NANSNVSILV---DDMMNVYRVKVLDPNOVEFQAF 50  
QY 108 REVAVSLQPVFEKAPPELLPFIKQIVPEPVITPFSVWLDDAGNLQNVRFVQVSSAIGP 167  
DB 51 HEIIVSLKPLFMEEPKXLPILITLSEPERAIQFVCHLDDNGVRKRCRVOYNALGP 110  
QY 168 YKGLRPHSVNLSIMKFLAEQIFKQSLTTLPMGGKGGSDPDKKSDAEVNRFCQSF 227  
DB 111 YKGLRPHSVNLSIVKFLGFEQIFKQSLTGLSWGKGGSDPDKKSDNEILKFCQAF 170  
QY 228 MTELQRIISVQVDPADIGVGAETGYLPGQYRIRKNTGVLTTPKQGEYGSSEIRPEA 287  
DB 171 MNELYRHIGPCTDVPADIGVGRIGLYLQYQKIVNSFNGTLTGKRVKGGSNLRVEA 230  
QY 288 TGYGAVLFVENVLKDKGESLKGRCLVSGAGNVQYCAELLLEKGAIVLSLSDSQYVYE 347  
DB 231 TGYGLVFLVEVLSLSLIPVEKQDAVVGSGSNVALYCVQKLLHNVKVLTLSDSNGYVYE 290  
QY 348 PNGFTREQLQAVODMKKKNNSARISEY--KSDTAVVYGDRRKPEWELDCOVDIAPPCATON 405  
DB 291 PNGFTHENLEFLDLKEE-KKGRITKEYLHNSSTAKYF-PNEKPMGVPC--TLAPPCATON 346  
QY 406 EIDEDHDELLIKGCGQYVVGAGNPNSTNEAIHKTKKGIICYCKKAAAGVAVSGLEMT 465  
DB 347 EIMNEDAKLLQKNCIIVGEGANPSTVDINLFKSNIIYCPSEKANNAGGVAISGLEMS 406  
QY 466 QNRSLMTREEVYDKLERIMKDIYDSAMGPSRYY---NVDLAAGNIAGFTKYADAVKA 522  
DB 407 QNPFQSWTRETVDKLEIKETIRNFIACSENALKYTKOKTDLQGANIAGFLKVAESYIE 466  
QY 523 QG 524  
DB 467 QG 468

RESULT 13  
Q923C4 PRELIMINARY; PRT; 445 AA.  
AC Q923C4;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE NADP-glutamate dehydrogenase (EC 1.4.1.4).  
GN Name=gdh;  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=PAOI;  
RA Ansaari F.;  
RL Thesis (1994), University of London, London U.K.  
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN 13  
RP SEQUENCE FROM N.A.  
RC STRAIN=PAOI;  
RA Brown P.R.;  
RT STRAIN (1994), University of London London U.K.  
RN 12  
RP SEQUENCE FROM N.A.  
RC STRAIN=PAOI;  
RA Ansaari F.;  
RL Thesis (1994), University of London, London U.K.  
EMBL: Y15166; CAA75437.1; -;  
DR EMBL: Y15166; CAA75437.1; -;  
DR HSSP; P24295; IAUJ.  
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro; IPR006095; GLFV\_dehydrog.  
DR InterPro; IPR006095; GLFV\_dehydrog\_C.  
DR InterPro; IPR006097; GLFV\_dehydrog\_N.  
DR Pfam; Pf00208; GLFV\_dehydrog\_1.  
DR Pfam; Pf02812; GLFV\_dehydrog\_N; 1.  
DR PRINTS; PR00082; GLFDHGRNAS.  
DR PROSITE; PS00074; GLFV\_DEHYDROGENASE; 1.  
DR Oxioreductase.  
KW SEQUENCE 445 AA; 48532 MW; B00DDEBE03A06D8A CRC64;  
SQ  
Query Match 47.2%; Score 1285; DB 2; Length 445;  
Best Local Similarity 58.4%; Pred. No. 2.3e-79;  
Matches 261; Conservative 56; Mismatches 118; Indels 12; Gaps 5;  
QY 86 VRQLLEIFPKDPQOEPMQAVNEVAVSLQPVFEKAPPELLP--IFKQIVPEPVITPFSV 143  
DB 5 VDAFLERLKRDPDQDEFHQAVEVLRSLMPLFLEANPHYLEAGIIRIVPERPAIIFRPV 64  
QY 144 WLDDAGNLQNVRFVQVSSAIGPYKGLRPHSVNLSIMKFLAEQIFKQSLTTLPMGG 203  
DB 65 WDDQGRVVRNCRVQWSSAIGPYKGLRPHSVNLSIMKFLAEQIFKQSLTTLPMGG 124  
QY 204 GKSGSDPDKKSDAEVNRFCQSFMTLQRIISVQVDPADIGVGAETGYLPGQYKRI 263  
DB 125 GKSGSDPDKKSDAEVNRFCQSFMTLQRIISVQVDPADIGVGAETGYLPGQYKRI 184  
QY 264 TKNYTGYLTPKQGEYGSSEIRPEATGYAVLFVENVLKDKGESLKGRCLVSGAGVAVQY 323  
DB 185 SNQFTSLTGKGLSYGSLTRPEATFGCYFAQEWLKKRGKGFDCQRAVISGSGVAVQY 244  
QY 324 CAELLLEKGAIVLSLSDSQYVYENPFTREQLQAVODMKKKNNSARISEYKSDT--AV 380  
DB 245 AAKRVMEGKATVLSLSDSSTGLTAEAGLSDEQWEYLMELK---NRRAGHPRGVEQFSL 300  
QY 381 YVGDRRKPEWELDCOVDIAPPCATONEIDEHDELLIKGCGQYVVGAGNPNSTNEAIHKYN 440  
DB 301 QPLEGVPPWGLAC--DIALPCATONELDAEDARRLLANGVCVAEGANPSTLEAVDLFL 358  
QY 441 KAGIICPGKAAAGVAVSGLEMTNRMSLMTREBVRDKLERIKDIYDS--MGPSRR 499  
DB 359 EAGIILVAPGASVAGVAVSGLEMSQANMRKLRWSBGEVDTKLGIQSIHRACTLYGEEQ 418  
QY 500 YNVDLAAGNIAGFTKYADAVKAQAV 526  
DB 419 GRVNYVKGANIAGFVYADMLAQGV 445

RESULT 14  
Q7YZU7 PRELIMINARY; PRT; 437 AA.  
AC Q7YZU7;  
DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Glutamate dehydrogenase (Fragment).  
GN Name=gdh;  
OS Trichomonas vaginalis.  
OC Eukaryota; Parabasallidae; Trichomonada; Trichomonadida;  
OC Trichomonadidae; Trichomonadinae; Trichomonas.  
OX NCBI\_TaxID=5722;  
RN 11  
RP SEQUENCE FROM N.A.  
RX PubMed=12820901; DOI=10.1186/1471-2148-3-14;  
RA Andersson U.O., Roger A.J.;  
RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes";  
RL BMC Evol. Biol. 3:14-14(2003).  
DR EMBL: AF533886; AAP83853.1; -;  
DR HSSP; P24295; IAUJ.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.



Query Match	47.2%	Score 1284.5	DB 2	Length 437
Best Local Similarity	59.0%	Pred. No. 2.4e-79		
Matches 255	Conservative 56	Matches 118	Indels 3	Gaps 2
QY	96	KDPEQGEOMAAREVAVSQIPFEKRPBELLPIFKQVDEERYTTFVSWLDDGNIQVNR	155	
DB	4	KDPDDKEETQATATEVLTSLVPTLEKEPKYQKLLPALVEBERVIMFVPVNDGEMVNR	63	
QY	156	GFRVYSSAIGPKYKGLRFPHPVSNLSIMKFLAEQIFKNSLTTLPMGGGKGSDFPFGK	215	
DB	64	GFRVGFNSAIGYKKGCRPRGNVNSILKFLFGEQVFNKSLTTLPMGGGKGSDFPFGK	123	
QY	216	SDAEVAFRCQSFMTLEORHISVYQDVPAQDIGVAREIGYLFQGYKRITKNYTGVLTPKG	275	
DB	124	SDGEVAFRCQSFMTLESRHIGNTQVPAQDIGVAREIGYMFQGYKRINVFEGVLTGK	183	
QY	276	QBYGSEETRPETATGAVLFEVNLKDKESLKGKGLVSGAGNVAQYCAELLEKGAIY	335	
DB	184	ISFGSLIRPEATYGLVYFVTEMLRAKEELKGRAMVSGSNVAQYCCQKLMQGAIP	243	
QY	336	LSLSQGVVVEPNQFTREQLQAVQDMKK-KNNSARISEYSDTAVY-VGDRKRMELD	392	
DB	244	VSCDSHGALLFKDQGTKEHLDAVMTIKVARTELKXISLELPDLKGYEYIDKSIWAC	303	
QY	393	COVIDAFPCATONEIDEHDAELLIKHCCQYVVEGANMPSSTNEAIHKYNRAGIYCPGKA	452	
DB	304	VPCMDGLCATQNELLPBHVPIVNVGNVYLLBEGANMPSSTNETIELYMENTIYFGGXAA	363	
QY	453	NAGYVAVSGLEMTQRMSLMNTREBYRDKLERIMKDIYDSANGPSRRYVNDLAAGNIA	512	
DB	364	NAGGVSVSGLEMTQNSVRLAWSSEKVDKLIKEMINIPEAASASASQYGVPLTKGANLAG	423	
QY	513	FTKVADAVKAG 524		
DB	424	FKRVADAVKAYG 435		
RESULT 15				
Q9TXS8				
ID	Q9TXS8	PRELIMINARY	PRT	442 AA.
AC	Q9TXS8			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, last annotation update)		
DE	Glutamate dehydrogenase.			
GN	Name=GDH;			
OS	Plasmodium falciparum.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX	NCBI_Taxid=5833;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
SC	STRAIN=FCQ 27;			
RA	Yuan P., Stewart T.S.;			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF098675; AAD11789.1; -			
DR	HSSP; P24295; 1AUP.			
DR	GO; GO:0016493; F:oxidoreductase activity; IEA.			
DR	GO; GO:0006520; P:amino acid metabolism; IEA.			
DR	InterPro; IPR006095; GLFV_dehydrog.			
DR	InterPro; IPR006097; GLFV_dehydrog.C.			
DR	InterPro; IPR006097; GLFV_dehydrog.N.			
DR	Pfam; PF00208; GLFV_dehydrog.N.1.			
DR	PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.			
FT	NON TER			
SQ	SEQUENCE 437 AA; 47861 MW; 75205554ADAFBE96 CRC64;			

DR	PROSITE: PS00074; GLFV DEHYDROGENASE. 1.	Score	46.5%;	Score 1265;	DB 2;	Length 442;
SEQ	SEQUENCE 442 AA: 49532 MW: 903FBA6F79CCE4CC CRC64;	Beat Local Similarity	59.8%;	Pred. No. 5,36-78;		
	Matches 258; Conservative 57; Mismatches 114; Indels 10; Gaps 6;					
QY	92 EIPMK-DPEQEFNOAVREAVNSIQPVFEKRELLPIFKQIVBERVITFPVSWLDDAGN	150				
Db	6 ERVKKLTDPNQVEFPAQFHEILYSLKPLFMEERKYLPIETLSEBERAIQFVVCWLDNDGV	65				
QY	151 LQNVRGPFVQVSSAIGPYKGLRPHSPVNLSIMKFLAPEQFKNSLTLLPMGGKGGSDP	210				
Db	66 QRKRCRFRVQNSALGPYKGLRHPNSNLSTVFLDEEQIFKNSLTGLSMGSGKGSDF	125				
QY	211 DPKKSDAEVRFQCSFMTLEQRIHSYVDVPADIDIGAREIGYLFQGYRITIKNTYGV	270				
Db	126 DPKGSDNEILKFCQAFNELYRIHIGCTDVPADIDGVGHQIGYLFQGYKLTNSFNGT	185				
QY	271 LTPKQEGVSGSEIRPEATGYGAVFVENVLTDKDESKLKKRCLTVSGAGNVAQCAELLLE	330				
Db	186 LTGNQVKKGGSNLRVEATGYGLVFLVEVLKSLNIPBEKQAVAVSSGNVALYCVQKLLH	245				
QY	331 KGAIVLSLSDSQGYVEBNGFTREQLQAVDDMKKNNSARISXY--KSDTAVVYVGDRRKP	388				
Db	246 LNVKVLTLTSDSNGVVEBNGFTHEINLEFLIDLKKE--KKGRIKETLNNSTAKYF--PNEKP	303				
QY	389 WELDCQVDIAFPCLATONSIDEBHDELLIKGCGQYVVEGAMNPSTNEAIHKTKNKAQIYCP	448				
Db	304 WGVPC--TLAFPCCATONEINLEDAKLIRKNGCIIIVGEGAMNPSTVDAINLFKSNIIYCP	361				
QY	449 GKANNAGVAVSGLEMTQNRKSLMTWTEBYRDKLERIMKOIYDSAMGSPRY--NDVLA	505				
Db	362 SKANAGGVALISGLEMSQNFQFSHTRETYDEKLEIMRNIFLACSENALKYTKYKYLQ	421				
QY	506 AGANIAGFTTKVADAVKAG 524					
Db	422 AGANIAGFTKVAESYIEDG 440					

Search completed: July 9, 2005, 18:35:05  
Job time : 185 secs

DR GO; GO:0016593; F:oxidoreductase activity; IEA.  
DR GO; GO:0006529; P:amino acid metabolism; IEA.  
DR InterPro; IPR006095; GLFV\_dehydrog.C.  
DR InterPro; IPR006096; GLFV\_dehydrog.C.  
DR InterPro; IPR006097; GLFV\_dehydrog.N.  
DR Pfam; PF00208; GLFV\_dehydrog\_1.  
DR Pfam; PF02812; GLFV\_dehydrog\_N\_1.  
DR PRINTS; PR00082; GLFVHDRGNASE.

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